AC108255 Rattus no

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 391 from Patent WOO2053141.
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Inhibition of angiogenesis by nucleic acids
patent: WO 02053141-A 391 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
Location/Qualifiers
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/mol type="unassigned DNA"
/db xref="taxon:32630"
/note="Synthetic oligonucleotide"
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                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
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90.0%; Pred. No. 83;
                                                                                         for DNA cytosine
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                                                                                                                                                                                                                                                    DB 6; Length 20;
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Matches
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                                                                                                                                             Local
                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cellular Biochemistry; Yayoi 1-1-1, B 113, Japan (B-mail:aa67146@hongo.ecc.u-tokyo.ac.jp, Tel:+81-3-9812-2111, Fax:+81-3-5689-7345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence updated (17-Sep-1998) Sequence updated (13-Jan-1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence updated Sequence updated
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Submitted (16-MAR-1998) Hiromichi Kimura, University of Tokyo,
Yavoi 1-1-1, Bunkyo-ku, Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 18,
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GGTACAGCCAGGACTACG 2696
                                       GGUACAGCCAGGACUACG
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVFDSNSSWFETYDSSPMKFTFFSVYCSRGHLCPVDTGLIERWELLYEGVAKAHE
ENPSVEGGVNGKULGE INQWATSGFDGGKALIGFSTAFASYFLMEBSPEYAPIFGLM
ENPSVEGGVNGKULGE INQWATSGFDGGKALIGFSTAFASYFLMEBSPEYAPIFGLM
QEKIYISKI VVERFLQSPDAVFEDLILIKITIONAETHATIVINSAKVKRKGFTKATI
TKLVYQIFDTFFSEQIEKDDKEBKENIMKRRRGGVCEVCQQPECGKCKACKJMVKEGG
TKLVYQIFDTFFSEQIEKDDKEBKENIMKRRRGGVCEVCQQPECGKCKKQNKDRISMLGE
PVKIEKTYYMKVSIDELFLYGECENMQLSYIFBSKKLHQGKKKKQNKDRISMLGE
PVKIEKTYYMKVSIDELFLYGECENMQLSYIFBSKVKVIYTRGFSPMAMBGGMDFBAH
WFCAGTDTVLGATSDPLELFILYGECENMQLSYIFBSKVKVIYTRGFSPMAMBGGMDFBAH
MFCAGTDTVLGATSDPLELFILYGECENMQLSYIFBSKVKVIYTRGFSPMKRSKRDFVNENF
LEQLEEKDGRYYSQDYARFESPFKTQPAEDNKHKFCLSCIRLLAELRQKEMPKV
LEQLEEKDGRYYCSSITKNGVYYRLGSVYYLPPEAFTFNIKMASPMKRSKRDFVNENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPRDTYRKYSDY I KGSNLDAPEPYR I GRIKEI Y CGKKKGGKVNEAD I KI RLYKFYRPE
NTHKS I QATYHAD I NLLYWSDEEAVVDFSDVQGRCTVEYGEDLLES I QDYSQGGPDRF
YFLEAYNSKTKS FEDPPNHARS PGNKGKGKGKGKGKGKGKPQVSEPKEPEAA I KLPKLRT
                                                                                                                                                                                                                                                                                                                                                                       LPEIQNGASAPEISYNGEPQSWFQRQLRGSHYQPILRDHICKDMSALVAARMRHIPLS
PGSDWRDLPNIQVRLRDGVITNKLRYTFHDTKNGCSSTGALRGVCSCAEGKTCDPASR
QPNTLIPWCLPHTGNRHNHWAGLYGRLEWDGFFSTTVTNPEPMGKQGRVLHPEQHRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGEVTNSLGQRLPQKGDVEMLCGGPPCQGFSGMNRFNSRTYSKEKNSLVVSFLSYCDY
YRPRFFLLENVRNSVSFRRSMVLKLTLRCLVRMGYQCTFGVLQAGQYGVAQTRRRAII
LAAAFGEKLFLEPEFLHVFAFRACQLSVVVDDKKEVSNITRLSSGPFRTITVRDTMSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGCPANGSRPTWKAMADSNRSPRSBKEROPRRSKSDSETMIEASSSSVATRRTTR
QTTITSHFKGPAKRKKEDSEKGNANESAAEBENDQKKGRVAGTESRASBAGESVEKF
GTVRGTQLCQEEQGSQEDDRRFRAQTRELASRRKSRBDDRBARFGTHLDVDDDDEK
ERVRFGTQLCQEEQGSQEDDRRFRAGTFELASRRKSRBDDRBARFGTHLDVDDDDEK
DKRSSRPRSQPRDJATKRRPKSEVEQITPEPPEGKDEDEREKRRKTTRKKPEPLSIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VQSRVERKASQGKASAI PKLNPPQCPECGQYLDDPDLKYQQHPVDAVDEPQMLTNEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLNLLHBFLQTEIKSQLCDLETKLHKEELSEEGYLAKVKTLLNKDLCLENGTLSLTQF
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/db_xref="taxon:10117"

/tissue_type="brain and placenta"

/dev_stage="adult"
                                                                                                                                                                                                                                                       /note="22 a nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="DNA cytosine 5 methyltransferase"
/protein_id="BAA37118.1"
/db_xref="GI:4160670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MPARTAPARVPALASPAGSLPDHVRRRLKDLERDGLTEKECVKE"
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                                                                                                                                       90.0%;
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                                                      19
                                                                                                            2
                                                                                                            Score 18; DB 9;
Pred. No. 5.6e+02;
2; Mismatches 0
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                                                                                                                                                                     Length 5253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (Charles Street, C., Lander, E., Abouelleil, A., Allen, N., Bartien, V., Blarna, N., Bastien, V., Blarna, N., Bastien, V., Bloukhgalter, B., Camarata, J., Chang, J., Choppell, Y., Collymore, A., Cooke, P., Corum, B., Choppell, Y., Collymore, A., Cooke, P., Corum, B., Charles, C., Collymore, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Parco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Grahham, L., Grand-Pierre, N., Hafez, N., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Muzhby, T., Macholad, P., Major, J., Manning, J., Matthews, C., Muzhby, T., Maylor, J., Meneus, L., Mihova, T., Mlenga, V., Muzhby, T., Naylor, J., Nguyen, T., Nicol, R., Norbu, C., Phunkhang, P., Pierre, N., Rachugha, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauber, S., Schupback, R., Stemback, R., Stephack, R., Stephack, S., Talamas, J., Tesfaye, S., Theodore, J., Theodore, J., Worket, T., S., Viel, R., Worket, T., Worket, T., S., Viel, R., Worket, T., Worket, T., S., Viel, R., Worket, T., Worket, T.
Submittee 1.2. Charles Street, Cambridge, MA 02141, USA Charles Street, Cambridge, MA 02141, USA On Jun 19, 2005 this sequence version replaced gi:44775767. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Stubbs, M., Vandataraman, V.S., Viel, R., Stubbs, M., Stubbs, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McBwan,P., McKernan,K., Meldrim,J., McConle,R., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Thododre,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Voung, C., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Topham, K., Travers, M., Vassiliev, H., Venkatar Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G.,
                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JUN-2005) Broad
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Birren,B., Linton,L., Nusbaum,C.
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Birren,B., Nusbaum,C. and Lander,B.
Mus musculus chromosome 8, clone RP24-187F1
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clone RP24-187F1 map 8, PROGRESS ***, 6 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
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Euarchontoglires; Glires; Rodentia;
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                        SEQUENCING IN
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COMMENT

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PEATURES
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AC135310
                                                                                                                         ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                            3 GUACAGCCAGGACUACGA 20
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                             AC135310.2 GI:24941813
AC135310.2 GI:24941813
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                          Rattus norvegicus clone CH230-11C16, ***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                      AC135310
                                                                                                                                                                                                                                                                                                         GTACAGCCAGGACTACGA 24556
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----- Project Information
Center project name: L26564
Center clone name: 187_F_1
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134990
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/db_xref="taxon:10090"
/chromosome="8"
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10936: gap of unknown length
41320: contig of 30384 bp in length
41420: gap of unknown length
101112: contig of 59692 bp in length
101212: gap of unknown length
104894: contig of 3682 bp in length
104994: gap of unknown length
134989: contig of 29995 bp in length
134989: gap of unknown length
135089: gap of unknown length
195617: contig of 57528 bp in length
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                                                                                                                                                                                                          243411 bp
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6, *** SEQUENCING IN PROGRESS
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REFERENCE

(bases 1 to 243411)

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Bryant, N., Bunay, U., Burcu, F., Burter, N., Cander, N., Cardens, V., Carter, K., Cawazos, I., Ceast, H., Center, A., Chu, J., Chacko, J., Chaves, D., Chen, G., Chen, R., Chen, Z., Chu, J., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Cockreil, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Dederich, D., Davia, K., L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, H., Davis, R., Deramo, E., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, H., Divya, K., Davis, R., George, R., Genter, M., Foster, M., Foster, M., Foster, M., Potter, M., Potter, M., Potter, M., Divya, K., Ding, R., Geris, M., Garra, M., Gerra, M., Gerra, M., Palagun, M., Forbes, L., Foster, M., Foster, M., Potter, M., Gunaratte, P., Hasland, M., Hamilton, C., Hamilton, K., Hallon, K., Hallon, J., Johnson, A., Hollins, B., Howells, S., Hulyk, S., Hand, J., Johnson, A., Hollins, B., Howells, S., Hulyk, S., Hand, J., Johnson, R., Jolivet, A., Karpathy, S., Kally, S., Kally, S., Khan, Z., King, L., Koyar, C., Karft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, Y., Lundon, P., Longacre, S., Lopez, J., Liu, Y., Lundon, P., Loyado, R.J., Malloy, K., Ma, J., Malloy, K., Ma, J., Malloy, K., Malloy, K., Ma, J., Malloy, K., 
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                   Submitted (13.NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 13, 2002 this sequence version replaced gi:23915440. On Nov 13, 2002 this sequence version replaced gi:23915440. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole sequence contigue to the contiguence of the contiguence of the contiguence as a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contiguence, and sequence contiguence contiguence and oriented, and sequence by sized gaps filled with Ns to the estimated size. The sequence by sized gaps filled with ns to the estimated size in the sequence that the sequence and the sequence that the sequence was the sequence of the contiguence and there may be sequence that the sequence of the contiguence and the sequence and the sequence that the sequence we will the sequence that the sequence was the sequence of the contiguence and the sequence was the sequence of the sequence and the sequence and the sequence of th
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3 (bases 1 to 243411)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/denbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record, will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 217795 bases at least Q40 Consensus quality: 222117 bases at least Q30 Consensus quality: 222117 bases at least Q20 Consensus quality: 224860 bases at least Q20 Estimated insert size: 223813; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: CH230-11C16
------ Summary Statistics
Assembly program: Phrap; version 0.990329
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complement(22562..23010)
/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
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lone_end:T7
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24604: gap of unknown length
97195: contig of 72591 bp in length
97295: gap of unknown length
210508: contig of 113213 bp in length
210608: gap of unknown length
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| . .26284
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28126: gap of unknown length
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                                                                  H.sapiens CpG island DNA genomic Msel fragment, read cpg70g5.ftlb.
                                                                                                                                                                                                                                                     μ
Z66016.1 GI:1038838
CpG island; genomic |
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-OCT-1995) The Sanger Centre, Hinxton, CB10 1RQ, England. B-mail contact: humquery@sanger.avector: pGEM-52f(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resource Centre, Hinxton, Cambridgeshihttp://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z61248.1 GI:1033626
CpG island; genomic
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="48h8"
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Pred. No. 1.
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Pred. No. 4.4e+02;
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Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MacDonald,M., Huckle,B., Wilkinson,P. and Micklem, Direct Submission
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                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 172415)
Cordum, H., Belter, E. and Mishra, S.
The sequence of Homo sapiens BAC clone unpublished (2001)
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AC073834
AC073834.6 GI:13677134
HTG.
                                                                                                   Submitted (23-MAY-2001) Genome University School of Medicine, MO 63108, USA
                                                                                                                                                                                                                                         Direct Submission
Submitted (29-UUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                   Waterston, R.H.
                                                                                                                                                                                                  MO 63108, USA
3 (bases 1 to 172415)
                                                                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC073834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGUACAGCCAGGACUACG 19
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                                                                                  (bases 1 to 172415)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="blood"
/clone_lib="CGI-1"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="70g5"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .275
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4;
Pred. No. 1.
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                                                                                                                           Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Bird, A.P.
a methylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from
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                                                                                                                                                                                                                                                                                                                                                                     RP11-250N10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
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On Apr 19, 2001 this sequence version replaced
On Apr 19, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-APR-2005) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping information for this clone was provided by Dr. Wes Warr
Department of Genetics, Washington University, St. Louis Mo. Pol
additional information about the map position of this sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: H_NH0250N10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                   join(1066..1127,6915...
31170...31373)
/gene="AGPS"
join(<1066...1127,6915.
                                                                                                                             /note="Homo sapiens alkylglycerone (AGPS), mRNA.; H_NH0250N10.1
This gene was based on g1(4501992)
Continued from H_NH0540F24.1"
                                                                                                                                                                                                                                                                                                                                    /gene="AGPS"
                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-250N10"
/clone_lib="RPCI-11"
                /translation="dlalbyyvlgespetsapwdrvvdlcrnvkeritreckekgvqf
appstcrvtqtydagaciypyfafnyrgisdpltvfeqteaaareeilanggslshhh
                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                   protein_id="AAX93112.1"
/db_xref="GI:62702186"
                                                                                          product="unknown"
                                                                                                                                                                                                                31170. .31291)
/gene="AGPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                     _xref="genomic DN
_xref="taxon:9606"
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                                                                                                                                                                                                  phosphate synthase
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For 998

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                                                                                                                                                                                                                                                                                                                                                                                               46163
         Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                    Mouse DNA
                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                   Direct Submission
                                                                                     Bray-Allen,S.
                                                                                                                                                                                                                                AL596108.13
                                                                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                                                                                                                     AL596108
                                                                                                                       sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                            musculus (house mouse)
                                                                                                                                                                                                                                                                              200966 bp DNA linear ROD 05-APR-2002 sequence from clone RP23-326K2 on chromosome 11, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRLLASTASSSPASVMVAKEDRN"
127515. .127784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="SMLMTACDLGAVTKPWEISRQVAELVTSEFFEQGDRERLELKLT
PSAIFDRNRKDELPRLQLEWIDSICMPLYQALVKVNVKLKPMLDSVATNRSKWEELHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This gene was based on gi(19923439)
Continued from H_NH0091J18.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(122503. .122658,156962.
162589. .162663,168551. .>168614))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CpG_island (%GC=61.2, o/e=0.88, complement (121180. .168614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="CpG_island (%GC=63.0, o/e=0.81, #CpGs=22)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAX93113.1"
db_xref="GI:62702187"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="CpG_island (%GC=63.1, o/e=0.95, 20153. .120428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Homo sapiens hypothetical protein FLJ13946 FLJ13946), mRNA.; H_NH0250N10.2.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="PDE11A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="FLJ30990"
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                                                                                                                                                                                                                                GI:20068503
                                                                                                                     tazoa; Chordata; Craniata; Vertebrata; Buteleostomi; heria; Euarchontoglires; Glires; Rodentia; Muroidea; Muridae; Murinae; Mus.
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162663,168551.
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LOCUS

product="16S ribosomal RNA"

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Submitted (13-FEB-2004) Microbial Ecology, University of Groningen, Kerklaan 30, Haren 9751 NN, The Netherlands Location/Qualifiers
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17; Conserv
                                                                                                                                                                                                                                                                                                       van der Wielen, P.W.J.J.
Direct Submission
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AY547816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                     Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                     anoxic Bannock basin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by the group of Pieter de Jong.
For further details see http://www.chori.or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pBACe3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the RPCI-23 Mouse PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-326K2 is
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                                                                              /mol_type="genomic_DNA"
/isolation_source="brine interface of Bannock basin,
Bastern_Mediterranean"
environmental_sample/
                            db_xref="taxon:77133"
clone="B42-25.0%"
                                                                                                                                                               organism="uncultured bacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-23"
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chromosome="11"
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mol_type="genomic DNA"
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89.5%;
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Bastern Mediterranean
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Pred. No. 8.
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8.7e+02;
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AY164354/c
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129 TACAGCCAGGACTACGA 113
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1 (bases 1 to 700)

1 (bases 1 to 700)

1 van der Wielen, P.W.J.J., Brons, J.K. and Bolhuis, H.

Bacterial and Archaeal Communities of 4 Deep-Sea Hypersaline Anoxic Basins in the Mediterranean Sea
Unpublished
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                                                                                                                                                                                         Uncultured Verrucomicrobia bacterium clone RNA gene, partial sequence.
AY164380
AY164380.1 GI:27371674
ENV.
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Direct Submission
Submitted (14-OCT-2002) CEES, University of Groningen, Laboratory
of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          4 UACAGCCAGGACUACGA 20
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1 (bases 1 to 700)

1 (bases 2 to 700)

1 (bases 3 to 700)

1 (bases 3 to 700)

1 (bases 5 to 700)

1 (bases 6 to 700)

2 (bases 7 to 700)

2 (bases 7 to 700)

2 (bases 7 to 700)

3 (bases 7 to 700)

4 Deep-Sea 1 Basins in the Mediterranean Sea
2 (bases 1 to 700)
van der Wielen, P.W.J.J.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol type="genomic DNA"
/isolation source="hypersaline anoxic basin; brine interface of L'Atalante, Mediterranean Sea"
/db xref="taxon:156588"
/clone="ALIB-68"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="uncultured Verrucomicrobia bacterium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="16S ribosomal
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88.2%;
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88.2%;
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Pred. No. 2e+03;
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Pred. No. 1.9e+03;
2; Mismatches 0
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                     Brons, J.K.
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Deep-Sea Hypersaline Anoxic
                        Bolhuis,H
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ALIB-68 16S ribosomal
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BLIB-55 16S ribosomal
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (14-OCT-2002) CEES, University of Groningen, Laboratory of Microbial Ecology, Kerklaan 30, Haren 9751 NN, The Netherlands Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AF011463
AF011463.1
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                                                                                                                                                                                                                                                                                                                                Submitted (30-JUN-1997) Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL St., Woods Hole, MA 02543, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monopylocystis visvesvarai N. Gen., N. Sp. and Sawyeria marylandensis N. Gen., N. Sp.: Two New Amitochondrial Heterolobosean Amoebae From Anoxic Environments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1908)
O'Kelly, C.J., Silberman, J.D., Amaral Zettler, L.A., Nerad, T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monopylocystis visvesvarai
Monopylocystis visvesvarai
Bukaryota; Heterolobosea; Monopylocystis
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Monopylocystis visvesvarai small
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Silberman,J.D., Roger,A.J., Nerad,T.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                            Similarity
                                                 TACAGCCAGGACTACGA 1091
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                                                                                                                                                                                                                                    /organism="Monopylocystis visvesvarai"
/mol_type="rRNA"
/strain="ATCC 50576"
/db_xref="ATCC:50576"
                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                        'product="small subunit ribosomal RNA"
                                                                                                                                                                                                                      'db_xref="taxon:63603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:4102252
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88.2%;
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88.2%;
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Pred. No. 1.9e+03;
                                                                                                                            Score 17;
Pred. No. 1
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                                                                                                                            1.8e+03;
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                                                                                                                                              DB 2;
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                                                                                                                                              Length 1908;
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AC160912/c LOCUS

DEFINITION

AC160912 177687 bp DNA linear F Rhinolophus ferrumequinum clone VMRC7-253D3, WORKING

HTG 04-MAY-2005

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC160912
AC160912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NISC Comparative Sequencing Initiative Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, E.D.
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Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhinolophus ferrumequinum (greater horseshoe bat)
Rhinolophus ferrumequinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: ijr
Center clone name: 253D03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 10.69x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 9.86x in Q20 bases; agarose-fp
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    Summary Statistics

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Cardenas,V., Caruz
Chavez,D.
                                              Muzny, D.Marie, Metzker, M.Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooka, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baidwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F. Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Cardenas, V., Cardena
                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Rattus.

1 (bases 1 to 191592)
                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
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***, 5 unordered riesss
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136063. .177687
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3885..33984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lone_end:SP6
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                       Chen,G., C
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 177687;
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IN PROGRESS
                                                                                                                                                      Benahmed, F.,
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Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eavee, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Frinsey, M., Flagg, M., Forbes, L., Foster, M., Garza, M., Garzer, T., Garza, M., Garzer, T., Garza, M., Garzer, M., Garzer, M., Garzer, M., Garzer, M., Garzer, M., Garzer, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., London, B., Lu, X., Ma, J., Ma, J., Lu, X., Ma, J., Lu, X., Ma, J., Lu, X., Ma, J., Ma, J., Lu, X., Ma, J., Ma, J., Lu, X., Ma, J., Ma, J., Ma, J., Lu, X., Ma, J., M
                                                                                                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Direct Submission

AL Submitted (11-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Oct 11, 2002 this sequence version replaced gi:21746209.

On Oct 11, 2002 this sequence version replaced gi:21746209.

On Oct 11, 2002 this sequence version of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecte/rar/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold individual sequence contigs are ordered and oriented, and sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 191592) TX Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                        shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 191592)
                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                Center code: BCM
                                                                                                                                                                   Center: Baylor
                                                                                                                                                                                                         -- Genome Center
                                                                                                                                                          College of Medicine
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REFERENCE AUTHORS TITLE

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AC154620

193801 bp

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linear

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TITLE JOURNAL

AUTHORS TITLE

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Matches
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                                          2 GGUACAGCCAGGACUAC 18
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NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
GGTACAGCCAGGACTAC 71749
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Center clone name: CH230-377A5
Center clone name: CH230-377A5
Center clone name: CH230-377A5
Center clone name: CH230-377A5
Assembly program: Phrap, version 0.990329
Assembly program: Phrap, version 0.990329
Consensus quality: 183102 bases at least Q40
Consensus quality: 184856 bases at least Q30
Consensus quality: 185893 bases at least Q20
Estimated insert size: 190794; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                            /note="wgs_end_extension
clone_end:T7"
144303. .145387
/note="wgs_end_extension
clone_end:T7"
145388. .145487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end_sequence:RXAWQ03TV*
139424. .140309
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="clone_boundary;lone_end:T7
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145487: gap of unknown length
146610: contig of 1123 bp in length
146710: gap of unknown length
148251: contig of 1541 bp in length
148351: gap of unknown length
151375: contig of 2924 bp in length
151375: gap of unknown length
151375: gap of unknown length
151375: gap of unknown length
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151276. .151375
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|46611..146710
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                                                                                                              85.0%;
88.2%;
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                                                                                                                                                                                                                                                                                                 _length=unknown
                                                                                           2
                                                                                         Score 17; DB 14; Length 191592;
Pred. No. 1.4e+03;
2; Mismatches 0; Indels 0;
                                                                                                  0
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SOURCE

Pieter de Jong and coworkers at http://www.chori.org

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REFERENCE
AUTHORS
TITLE
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The BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or
                                                                                                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems,
                                                                                                                                                                                             SOURCE INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                              MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence from the Mouse Genome Sequencing Consortium whole guenorium may have been used to obtain the consensus sequence. assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
                                                                                                                                                                                                                                                                      http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mouse genome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all regions were double stranded,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JAN-2005)
Parkway, St. Louis, MO
4 (bases 1 to 193801)
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Submitted (30-DEC-2004)
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Trani, L. and Cotton, M.
The same continuous same contin
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AC154620 AC120857
AC154620.2 GI:71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE:
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Direct Submission
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Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aug 3, 2005 this sequence version replaced gi:56900246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 193801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: M BA0323M20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
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AUTHORS
TITLE
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KEYWORDS
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61853
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
                                                                                      Comenstry: Dye-terminator; 100% of reads Consensus quality: 192076 bases at least Q40 Consensus quality: 192699 bases at least Q30 Consensus quality: 193232 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                          On Aug 3, 2005 this sequence version replaced gi:71793983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
coverage: 7.84x in Q20 bases; agarose-fp
                    Insert size: 193739; sum-of-contigs
Insert size: 193745; 4.7% error; agarose-fp
Quality coverage: 7.84x in Q20 bases; sum-o
                                                                                                                                                                         Assembly program: XGAP4; version
                                                                                                                                                                                                                          Center project name: bM35905
                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                   Center code: SC
                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CT025535.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus chromosome 14 clone RP23-35905, *** PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CT025535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the entire insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUACAGCCAGGACUACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 194439)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (house mouse)
                                                                                                                                                                                                   ----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="Unresolved simple sequence repeat."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Unresolved homopolymeric repeat.
.72159. .172248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Unresolved simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP23-323M20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:71793992
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    Project Information

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88.2%;
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Pred. No. 1.4e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the clone.
                    sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193801;
                                                                                                                                                                                                                                                                                                                                                                                                                           vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCING IN
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NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is

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ACCESSION
VERSION
KEYWORDS
                                                                                           RESULT 19
AC108255
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                                                                  DEFINITION
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Best Local Similarity
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AC108255
AC108255.5 GI:30580587
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                               AC108255 252467 bp
Rattus norvegicus clone CH230-29E2,
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be
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                                                    4 unordered pieces.
                                                                                                                                                                                    GUACAGCCAGGACUACG 19
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43405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment_
86508. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00748
fragment_chain:1
clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:00476
fragment_chain:1"
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43405. 70409
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:01224
fragment_chain:1"
166131 .177242
                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00354
fragment_chain:1"
187836...194439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"

mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                 vector_side:right"
                                                                                                                                                                                                                                                                                                                                                                                           fragment_chain:
177343. .187735
                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:00235
fragment_chain:l"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00152
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment:00073
fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:00001
fragment_chain:1
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86407: contrig of 8905 bp in length
86507: gap of 100 bp
166030: contrig of 79523 bp in length
166130: gap of 100 bp
177242: contrig of 11112 bp in length
177342: gap of 100 bp
187735: contrig of 10393 bp in length
187835: gap of 100 bp
197835: gap of 100 bp
194439: contrig of 6604 bp in length
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70509: gap of
77402: contig
                                                                                                                                                                                                                              85.0%;
88.2%;
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contig of 27005 bp in length
                                                                                                                                                                                                                              Score 17; DB 14;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 43304 bp in length
                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                               Length 194439;
                                                                      SEQUENCING
                                                                         HTG 13-MAY-2003
IN PROGRESS ***,
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AUTHORS
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ORGANISM
                                                                                                                                                                                            TITLE
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                             Worley, K.C
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Mitaryota, Wetaroa, Chordata; Cranista; Vertebrata, Ruceleostomi, Mammadia; Butheria; Buarchontoglires; Goltres; Rodentia, Manmadia; Butheria; Buarchontoglires; Goltres; Rodentia, Manmadia; Butheria; Butherhontoglires; Goltres; Rodentia, Marchae, Martinae, Martinae,
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DEFINITION
ACCESSION
                                                                                                                                    RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
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                                                                                        Pocus
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                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                           69203
720 bp DN.
Pseudomonas aeruginosa gene for Lask,
D30812
D30812.1 GI:541656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                        GTACAGCCAGGACTACG 69219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.); NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                        GUACAGCCAGGACUACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GLFP
Center clone name: GLFP
Center clone name: GH230-2982
Center clone name: CH230-2982
Assembly program: Atlas 3.0;
Consensus quality: 232152 bases at least Q40
Consensus quality: 234728 bases at least Q30
Consensus quality: 234622 bases at least Q30
Consensus quality: 236632 bases at least Q30
Estimated insert size: 242175; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_contig"
247031. .247130
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                                                                                                                                                                                                                                                                                                                                                                                                                             estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                    estimated length=unknown 50349. .250448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="CH230-29E2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                             85.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                          Score 17; DB 14;
Pred. No. 1.4e+03
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                                                          complete cds
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                                                                                   linear
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                                                          KEYWORDS
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Best Local :
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                                                                                                                                                                                                                            124
     Bacteria;
                   Pseudomonas aeruginosa
                                      Pseudomonas aeruginosa
                                                                           D30813.1
                                                                                                           Pseudomonas aeruginosa gene
                                                                                                                                PSELASRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fukushima,J., Ishiwata,T., Kurata,M., You,Z. and Okuda,K.
Intracellular receptor-type transcription factor, LasR, contains
highly conserved amphipathic region which precedes the putative
helix-turn-helix DNA binding motif
Nucleic Acids Res. 22 (18), 3706-3707 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax:81-45-787-2509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-MAY-1994) Jun Fukushima, Yokohama City University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gambello, M.J. and Iglewski, B.H.
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       School of Medicine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanazawa-ku,, Yokohama, Kanagawa 236, J
(B-mail:jfukusim@med.yokohama-cu.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .902216
                                                                                                                                                                                                                          AAGGACAGCCAGGACTACGA 143
                                                                                                                                                                                                                                                               AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 720)
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                                                                                                                                                                                                                                                                                                                                                                                         /citation=[1]
/replace="g"
                                                                           GI:541658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDYENAFI VGNYPAAWREHYDRAGYARVDPTVSHCTQSVLFI FWEPSI YQTRKQHEFF
BEASAAGLVYGLTMPLHGARGELGALSLSVEAENRAEANRFI ESVLPTLMMLKDYALQ
Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="lasR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="lasR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MALVDGFLELERSSGKLEWSAILQKWASDLGFSKILFGLLPKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="BAA06489.1"
db_xref="GI:541657"
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strain="IF03455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="transcriptional activator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="pBTaclasR3455"
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                                                                                                                                                                                                                                                                                                                   84.0%;
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                                                                                                                                                                                                                                                                                                                   Score 16.8;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                             720 bp
                                                                                                             Lask, complete cds.
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                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                DNA
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p, Tel:81-45-787-2602;
                                                                                                                                                                                                                                                                                                                                   Length 720;
                                                                                                                                BCT 21-JAN-2003
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BD224017
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Fukushima,J., Ishiwata,T., Kurata,M., You,Z. and Okuda,K.

Fukushima,J., Ishiwata,T., Kurata,M., You,Z. and Okuda,K.

Intracellular receptor-type transcription factor, LasR, contains a highly conserved amphipathic region which precedes the putative helix-turn-helix DNA binding motif
helix-turn-helix DNA binding motif
Nucleic Acids Res. 22 (18), 3706-3707 (1994)
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                                                                                                                PATENT TO 2002522079-A 16 23-JUL-2002;

SYNGENTA LTD
OS Pseudomonas aeruginosa
PN JP 2002522079-A/16
PN 12-AUG-1999 JP 2000565139
PF 12-AUG-1999 GB 9817704.1
PR 13-AUG-1998 GB 9817704.1
PR 13-AUG-1998 GB 9817704.1
PN 13-AUG-1999 GB 9817704.1
PN 13-AUG-1998 GB 981704.1
PN 13-AUG-1998 GB 981704.1
PN 13-AUG-1998 GB 981704.1
PN 13-AUG-1
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Gene
FT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 720)
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Pseudomonas aeruginosa
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ODYEMAFIVCHYPAAWREHYDRAGYAKVDFTVSHCTGSTLDIFWEFSIYQTTKQHEFF
EBASAAGLVYGLTMPLHGARGELGALSLSVEBAURAEAURAEFIESVLFTLMMLKUYJLO
SGAGLAFEHFVSKFVVLTSWEKEVLQWCAIGKTSWEISVICNCSEAUVNFHMGNIRKK
FGVTSRRVAAIMAVNLGLITL"
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/mol_type="genomic DNA"
/strain="PA103"
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/transl_table=11
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Pred. No. 2.
   /organism='Pseudomonas
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CQ839858.1
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Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                            Pseudomonas aeruginosa
Bacteria; Proteobacteria;
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Feesche, J., Stumpe, S., Maurer, K.H., Breves, R. and Hoven, N. Method for controlling processes based on microbial interaction
                                              Pseudomonadaceae; Pseudomonas.
                                                                                          Pseudomonas aeruginosa
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/mol_type="unassigned DN
/db_xref="taxon:287"
1. .720
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/mol_type="genomic DNA"
/db_xref="taxon:287"
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/procein_id="CAH05768.1"
/db_xref="GI:50837796"
/db_xref="GI:50837796"
/db_xref="GI:50837796"
/translat.ton="MALVDGFLELERSSGKLEWSAILQKMASDLGFSKILFGLLPKD8
/translat.ton="MALVDGFLELERSSGKLEWSAILQKMASDLGFSKILFGLLPKD9
/translat.ton="MALVDGFLELERSSGKLEWSAILQKMASDLGFSKILFGLAWALKDYALQ
QYBAGLAFERPYSKPVLISREKEVLQWCAIGKTSWEISVICNCSEANVNFHMGNIRK
FGVTSRRVAAIMAVNLGLITL"
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Pred. No. 2.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Pharmacology, Harvard Institute of Proteomics, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
This clone is part of the Pseudomonas aeruginosa PAOI ORF clone collection generated by the Harvard Institute of Proteomics. Each CDS has been PCR-amplified from genomic DNA. Initiation codon has been normalized to ATG and stop codon has been substituted for GGA to allow generation of C-terminal tagged proteins. AttB recombination sites have been added to either end of the orf and attaction of the companion 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                        directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'GAAGGAGATACC' before t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qiu,Q., Anumanthan,A., Mar,W., Zuo,D., Taycher,E., Halleck,A., Hainsworth,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic construct Peudomonas PA1430 gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (15-JUN-2004) Biological Chemistry and Molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taycher, E., Halleck, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Pseudomonas aeruginosa gene repository
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                     /clone="FLH052756.01F"
/lab_host="Becherichia coli DH5alpha T1 resistant"
/note="derived from Pseudomonas aeruginosa"
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QDYENAFIVGNYPAAWREHYDRAGYARVDPTVSHCTQSVLFIFWEFSIYQTRKQHEFF
EBASAAGLVYGLTWPLHGARGELGALSLSVEAENRAEANRFWESVLFTLWMLKDYALQ
                                                                                                                              db_xref="taxon:32630"
                                                                                                                                                                                          organism="synthetic
                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGVTSRRVAAIMAVNLGLITL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGAGLAFEHPVSKPVVLTSREKEVLQWCAIGKTSWEISVICNCSEANVNFHMGNIRRK
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db_xref="GI:50837800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Pseudomonas aeruginosa"
|mol_type="unassigned DNA"
|db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                          _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mar,W., Zuo,D.,
Hainsworth,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                            binding site and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    명
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murthy, T.V.S.,
Lory, S., LaBaeı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murthy, T.V.S., Hu, Y., Lory, S., LaBaer, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .V.S., Hu,Y.,
LaBaer,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLH052756.01F
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Michael C. Zody
Broad Institute of MIT and Harvard
                                          SNQS(30,25)(single strand NQS, base in question has Phred sco
                                                                                calls must have Phred score >= 20, at least 30% of its base calls must satisfy
                                                                                                                           chimpanzee SNP discovery, read must be at least 500
                                                                                                                                                                                                                                                    troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pan troglodytes troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                      the read have Phred
                                                                                                                                                                   troglodytes troglodytes is the central chimp.
                                                                                                                                                                                                                                                                                                                                         the Human genome NCBI
Build 34 (hg16,July 2003). Chimp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mczody@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jaffe,D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Pan.
1 (bases 1 to 802)
Mikkelsen, T.S., Hillier, W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BV638815.1 GI:62628993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S216P61354FA6.T0 Masuku
                                                                                                                                                                                       estern chimp and
                                                                                                                                                                                                                                                                                                                                                                               23,021,928 chimpanzee whole genome shotgun reads were aligned to
                                                                                                                                                                                                                                                                                                                                                                                                                              STS size: 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: No sequence submitted
Primer B: No sequence submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Initial Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                              Gon, Unknown Chimp)
                                                                                                                                                                                                                                                                                                                       ncluding Clint (Pan
                                                                                                                                                                                                                                                                                                                                                                                                              rococol:
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                                                                                                                                                                                                                                      unknown origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 troglodytes troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QDYENAFIVGNYPAAWREHYDRAGYARVDPTVSHCTQSVLFIFWEPSIYQTRKQHEFF
EBASAAGLVYGLTMPLHGARGELGALSLSVEAENRAEANRFWESVLPTLWMLKDYALQ
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FGVTSRRVAAIMAVNLGLITLG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="PA1430"
/protein id="AAT50467.1"
/db xrof="Gi149082134"
/trānslation="MALVDGFLBLERSSGKLEWSAILQKWASDLGFSKILFGLLPKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /replace="t"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
|transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
and the read must have at least 200 bp SNQS(30,25)
                                                                                                                         least 500bp in length, at least 50% of its base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cambridge,
                                                                                                                                                                                                                Common names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 11
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                          score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bichler, B.B., Zody, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MA 02141,
                                          ĭ
                                                                                                                                                                                                                                                                                                                                           WGS reads were from 9
                                        30,
                                                                                                                                                                                                              Pan troglodytes verus is the
                                      the surrounding 10 bases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 720;
                                                                                                                                                                     To be included in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                      chimps
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placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NQS(30,25) standard was a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping reads to call NQS bases and SNPs. Alignments (between two reads) with less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         placed at the same locus of human genome) were discarded.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignments (>=95% bases of read A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
RsaL (rsaL)
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1138 to 1380)
de Kievit, T., Seed, P.C., Nezezon, J., Passa
RsaL, a novel repressor of virulence gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cloning and characterization of the Pseudomonas aeruginosa gene, a transcriptional activator of elastase expression J. Bacteriol. 173 (9), 3000-3009 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M59425.1 GI:151325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gambello, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                          Submitted (09-MAY-1991) Microbiology and Immunology, University of Rochester Medical Center, 601 Elmwood Ave., Rochester, NY 14642,
                                                                                                                                                                                                                                                                Gambello, M.J. and Iglewski, B.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                           1902216
                                                                                                                                                                                                                                                                                                                            10094696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGCACAGCCAGGACTAAGA 51
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                                                                                                                                                                                                                                                                                                                                                Bacteriol. 181 (7),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bases 1 to 1725)
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                                                                                                                                                                                                                                                                                                      bases 1 to 1725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Pan troglodytes troglodytes"
/mol_type="genomic_DNA"
/sub_species="troglodytes"
/db_xref="taxon:37011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1725 k
s aeruginosa lask (l
) genes, complete cd
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                   organism="Pseudomonas aeruginosa"
/gene="lask"
/function="activate elastase expression"
                                                     'gene="lask"
                                                                                         db_xref="taxon:287"
                                                                                                                 strain="PAO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.0%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Iglewski, B.H.
                                                                         .1148
                                                                                                                                   type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                  2175-2184 (1999)
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(lask)
cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                           Passador, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virulence
                                                                                                                                                                                                                                                                                                                                                                                       ador, L. and expression
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                                                                                                                                                                                                                                                                                                                                                                                           Iglewski,B.H.
in Pseudomona
                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas
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VERSION
KEYWORDS
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APGUCYC
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="rsaL"
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ITSWYNADNSQGTGPPSAGAFPLAIQYANNDDILHGYDINEBWPUTHCHIRIPPS
SDWWKRGFLGVIGPGGCCTYEGRLASALNFPMLDYACDENPVSNKEFYPTFLRTIPPS
SDWWKRGFLGVIGPGGCCTYBGRLASALNFPMLDYACDENPUSHEEMBILHEBYYAGFD
IQVVDSILLTILMYDMNQVTVVVBNITKYRNVFNTWKKQFDMREEMBILHEBYYAGFD
IQVDSILLTILMYDMNQVTVVVBNITKYRNVFNTWKKQFDLRGFDLRGFDAIDVGILNSGDYAIVGAVI
PWDPDAABPFTDIIQRYKKTTRIYVFFGDSGDLRQFAISALDVGILNSGDYAIVGAVI
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                 dletrdsqdyhsleytleasdyleqinqayeqmfklreytrtdderalbamksvlivt
                                                                                                                                                                       db_xref="GI:5649"
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85.0%;
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RESULT 27 PSELASR

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KEYWORDS

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Arbacia punctulata (punctuate urchin)
Arbacia punctulata
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Sea urchin (Arbacia punctulata)
                                                                                                                                                                                                                                                                                                             Singh, S., Lowe, D.G., Thorpe, D.S., Rodriguez, H., Kuang, W.J., Dangott, L.J., Chinkers, M., Goeddel, D.V. and Garbers, D.L. Membrane guanylate cyclase is a cell-surface receptor with homology to protein kinases Nature 334 (6184), 708-712 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Arbacoida; Arbaciidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="maludgflblerssgklewsailokmasdlgfskilfgllpkds
QDYEMAFIVGNYPAAWREHYDRAGYARVDPTVSHCTQSVLFIFWEPSIYQTEKQHEPF
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SGAGLAFEHPVSKFVVLTSREKEVLOWCAIGKTSWEISVICNCSEANVNFHMGNIRRK
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/protein id="AAA25874.1"
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/trans1 table=11
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                                                                                                                                                                                        /organism="Arbacia punctulata"
/mol_type="mRNA"
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/protein_id="CAA31367.1"
                                                                                                                  tissue type="testes"
/clone lib="lambda-ZAP"
                                                                                                                                                             db_xref="taxon:7641"
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Pred. No. 2.3e+03;
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                                                               COMMENT
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This represents the February 3, 2003 version of the continually updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation
                                                                                 Biochemistry, Simon Fraser University, 886
Burnaby, British Columbia V5A 186, Canada
                                                                                                        Submitted (04-FBB-2003) Department of Molecular Biology and Biochemistry, Simon Fraser University, 8888 University Dr.,
                                                                                                                                                                                                                                                                             Submitted (16-MAY-2000) Department of Medicine and University of Washington Genome Center, University Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                         Stover.C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,B., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu.Z., Paulsen,I.T., Reizer,J., Saier,M.H., Hancock,R.B.W., Lory,S. and Olson,M.V.
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                                                                                                                                                                        Direct Submission
                                                                                                                                                                                         Pseudomonas aeruginosa Community Annotation Project (PseudoCAP)
                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Nature 406 (6799), 959-964 (2000)
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AE004572.1 GI:9947372
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Similarity 85.0%;
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QAGGDMYDGSQVVSNLENTSYRSKAKADYQPDENGDGVKSYVLLHRIPIPVGDGGMPP
GSPGMYPIGTPVRAESGHWSPNKDYDLLNEWHNRDDPLLMMPVCGFHGELCTNWGLYL
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VLSAISVISNAEKQQIFATIGTYRGTICALHAVHKNHIDLTRAVRFELKLAFRAMRHIN
ICPFIGACIDRPHICILMHYCAKGSLQDIMENDDIKLDSMFLASLIADLVKGLVYLHS
SEIKSHGHLKSSNCVVDNRWVLQTTDYGLHEFRKQKEDVDLGEHAKLARKLWTAPEH
LREGKSMHPGGTPKGDIYSFSILTFENKSRQBFPHENDLELADIIARVSKEVPPYRP
VLNAVNEAAPDCVLTAIRACWVEDPMERENIIEWTMLAFLQKGLKPNILDNMIATHE
RYTNNLEELUDERTQELQKEKAKTEQLLHRMLPPSIASQLIKGISVLPETFDMVSIFF
SDIVGFLHFSLSSCRLECSSQVLPLLVPWLHSLLTLPLHLPLIWMPLISSFAQPSW
CNIUNGGCONIUGS
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204. .3098
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Pred. No. 2.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class
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3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: Punction experimentally demonstrated in P. aeruginosa.
2: Function of highly similar gene experimentally demonstrated in another organism (and gene context consistence).
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4: Homologs of previous?
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                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAG04814.1"
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/translation="mynystiftldgysfqlpdgsllfsdldgyrpwlealariea
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KSLLADYBCLGERWDIRQRLADALAABGLGHRADJFSERLSGGECWRVALLGAFLD
DADFLILDSSCHLDGAFALLRARLAMDGGLLIVSHDRELLEGMORIVELGTIGLE
DADFLILDSSCHLDGAFALLARLAMDGGCLLIVSHDRELLEGMORIVELGTIGLE
SYGGGYSFYAQSREBAREAAERRLDQRRLBRKRQTLAMREQQQRQERCQASGRREGKT
/note=^{-}Protein name confidence: Class 4 (homologs previously reported genes of unknown function, or similarity to any previously reported sequences) **
                                                                                                                                                                                                                                                                                ANQAKILLGGFRERGEVSAGKLRNAHQABBERLDREVREAAREVEBASPILLIDSPDAB-
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QPCATLSGGERLKAALALVLYADRPAQLLLLDBPDNHLDLAARQALESMLGQYRGALL
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                                                                                                                                                                                                                                                       VVSHDPVFLRHLALDGELRATAAGWRLEDR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / translation="Mprircercarpashcicalipsipsrrvlvlohpsswghaln
Taglavlglchaelkwgerpaestwrvpgyraclipsggaralaewaarbageplil
VVDDGTWRKARKLHINPALAALPRWSLAEGWASRYRIKKAPCEGALSTIBAIAAALD
ELEAPRTHEALLKPPDALIEGQIAAWGEDTYRRNHLSQERRRR"
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//note="Protein name confidence: Class 4 (homologs previously reported genes of unknown function, or similarity to any previously reported sequences)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
/transl table=11
/product="pubable ATP-binding component of ABC
transporter"
                                                                                                               locus_tag="PA1426"
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transl_table=11
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937. .3293
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280. .2896
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product="hypothetical protein"

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/na. .8016
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/codon_start=1
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Udyneqneqagefyrhygergtgrsatdsagrpefllhmsl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                            PPLQALFGSVGLAPGEWARVLLAGLGLFCVAELEKWLCRRVRARQA"
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VERSION
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AC016208
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, S., Alleu, N., S., Birren, B., Linton, L., Nusbaum, C., Lander, S., Alleu, N., Berckerly, R., Boguslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Collymore, A., Collymore, A., Collymore, A., Collymore, A., Collymore, A., Donnore, R., Collymore, A., Donnon, C., Dearellano, K., Domino, M., Donelan, L., Doyle, M., Core, P., Pinke, R., Gage, D., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Klein, J., Howland, J., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., McClaughlin, J., Marquis, N., McKernan, K., McClaughlin, J., Marquis, J., Morman, C.H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Petterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Petterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirreil, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, M.J., Zimmer, A. and Zody, M.
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Birren,B., Linton,L., Nusbaum,
Homo sapiens, clone RP11-25L11
                                                                                                                                                                                                                                                                                                                   Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 14, 2000 this sequence version replaced gi:6910681. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html http://ftp.genome Center Genome Center Whitehead Institute/ MIT Center for Genome Research Center: Whitehead Institute/ MIT Center for Genome Research
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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Homo sapiens clone RP11-25L11, V
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(bases 1 to 36255)
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Sgaglafehpvskpvvltsrekevlqwcaigktsweisvicncseanvnfhwgnirrk
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/transl_table=11
/product="transcriptional regulator Lask"
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Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lander, E., Allen, N., Anderson, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear HTG 14-MAY-2000
DRAFT SEQUENCE, 5 unordered
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RESULT 31
AL161661
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                  ORGANISM
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                                                                                                                                                                                                                 14190
                                                                                                                                                                                                                                                                                      16;
                                                                                     93714 bp DNA 1
Homo sapiens chromosome 20 clone RP5-984I23.
AL161661
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      Homo
                                                AL161661.1 GI:7263577
HTG; HTGS_PHASE2; HTGS_CANCELLED
                                                                                                                                                                                                                 AGGTACAGCCAGGAGTAAGA 14209
                                                                                                                                                                                                                                    AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 21.9 in Q20 bases; agarose-fp Quality coverage: 17.7 in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 29000; agarose-fp Insert size: 35855; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 35779 bases at least Q20
                    sapiens
                                 sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                            estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                       'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                estimated_length=100
7267. .24683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rector_side:right"
7167. .17266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment
lone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  estimated_length=100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RP11-25L11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one_end:T7
                                                                                                                                                                                                                                                                                                   84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imated_length=100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lib="RPCI-11 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194: contig of 5294 bp in length
194: gap of 100 bp
181: contig of 5487 bp in length
181: gap of 100 bp
186: contig of 6185 bp in length
186: gap of 100 bp
188: gap of 100 bp
188: contig of 7417 bp in length
188: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qualifiers
                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                    Score 16.8;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                    .9e+03;
                                                                                                                                                                                                                                                                                                                   DB 14;
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                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                     Length 36255;
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                                                                                                                        HTG 13-JUN-2001
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ACCESSION
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KEYWORDS
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AUTHORS
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AC166715/c
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Best Local
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 111051)

1 (bases 1 to 111051)

Mizny, D., Adams, C., Agbai II, O., Allen, C., Alsbrooks, S., Archer, P., Arredondo, H., Bandaranaike, D., Bangura, L., Beltran, B., Beltran, R., Beraducci, A., Biswalo, K., Blyth, P., Bonham, H., Buhay, C., Burch, P., Cadoree, I., Canada, A., Cardenas, V., Carter, K., Cavazos, I., Chaber, T., Chaber, M., Carder, K., Cavazos, I., Chaber, J., Chabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus clone CH240-190KB, ***
unordered pieces.
                                          Chacko, J., Chahrour, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC16671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC16671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (12-UNN-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (12-UNN-2001) Sanger Centre, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 93714; sum-of-contigs
Insert size: 109355; 1.0% error; agarose-fp
Quality coverage: 8.25x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 93681 bases at least Q40 Consensus quality: 93706 bases at least Q30 Consensus quality: 93713 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid, L08752, 100% of reads Chemistry: Dye-terminator Big Dye, 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: dJ984I23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence will be replaced
by the finished sequence as so
the accession number will be pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGUACAGCCAGGACUACGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1715.2 GI:72095138
HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the finished sequence as soon as it is accession number will be preserved.
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chromosome="20"
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clone_lib="RPCI-5"
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.8;
Pred. No. 1.
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                                          Chavez, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCING
          Chen, A., Chen, G., Chen, R., krell, R., Coyle, M., Cree, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available and
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Cree, A.,
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Anda.C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Durn,A., Durbin,K., Driuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M., Perrandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fernando,P., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fowler,G., Fu,Q., Fhh,E., Garcia,A., Garcia,R., Garrier,T., Gench,S., Gench,S., Gill,R., Gorzalez,D., Hall,B., Hand,H., Hamilton,K., Harbes,B., Harris,R., Havbas,B., Hollins,B., Hawkins,E., Havbas,S., Heme,J., Imo,K., Jackson,A., Jackson,L., Jang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S., Jacob,I., Jiang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S., Leak,S., Lee,K., Lee,S., LeGall,R.I., Li,X., Kelly,S., Leak,S., Lee,K., Lee,S., LeGall,R.I., Li,X., Li,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-AUG-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 10, 2005 this sequence version replaced gi:71834693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-AUG-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
Center project name: FXVI
Center clone name: CH240-190X8
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 123099 bases at least Q40
Consensus quality: 123099 bases at least Q30
Consensus quality: 130502 bases; sum-of-contigs estimation
Bstimated insert size: 143053; agarose-fp estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 111051)
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. The true order of the pieces
                                                                             NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 111051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is not known and their order in this sequence record is
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/db_xref="taxon:9913"
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6573: contig of 2328
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8716: contig of 2043
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KEYWORDS
SOURCE
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AC073138
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  18 (bases 1 to 118396)

18 Hillier, L.W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Wylie, K., Sekhon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delchaunty, K.D., Miner, T.L., Nash, W.E., Coordes, M., Du, H., Sun, H., Edwards, J., Bradshaw-Cordum, H., Ali, J., Andrews, S., Isak, A., Vanbrunt, A., Nguyen, C., Du, F., Lamar, B., Courtney, L., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Kalicki, J., Ozersky, P., Bielicki, L., Scott, K., Holmes, A., Kalicki, J., Ozersky, P., Bielicki, J., Scott, K., Holmes, A., Rohlfing, T., Harkins, R., Harris, A., Strownstt, C., Scott, K., Hou, S., Tomlinson, C., Daughin-Kohlberg, S., Kozlowicz-Reilly, A., Leonard, S., Rohlfing, T., Rock, S. M., Tin-Wollam, A.M., Albott, A., Minx, P., Maupin, R., Strownstt, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woessmer, J.P., Wendl, M.C., Yang, S.P., Schultz, B.R., Wallis, J.W., Spieth, J., Bieri, T.A., Nelson, J., Berckwicz, N., Wohldmann, P.E., Spieth, J., Bieri, T.A., Nelson, J., Warra, M.A., Raymond, C., Mardis, B.R., Clifton, S. W., Chissoe, S. L., Warra, M.A., Raymond, C., Hubb, K., Stmen R., Lay, P., Clonden, T., Phelps, K., Iadanoto, S., Hubb, K., Stmen R., Faller, J., Wans, R., Phelps, K., Iadanoto, S., Hubb, K., Stmen R., Lay, P., Clonden, R., Phelps, K., Iadanoto, S.,
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University, 4444 Forest Park Avenue, St. Louis
On May 9, 2001 this sequence version replaced
                                                                                                                                                                                            Submitted (31-JAN-2004) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
                                                                                                                                                                                                                                                 Wilson, R.
Direct Submission
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Submitted (09-MAY-2001)
University, 4444 Forest
(bases 1 to 118396)
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Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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The sequence of Homo sapiens
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Nature 424 (6945), 157-164 (2003)
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  Center project
                   Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
Summary Statistics
                                                                                                   Center code: WUGSC
                                                                                                                         Center: Washington University Genome
                                                                                                                                                  ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
name: H_NH0708P17
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                                                                                                                                                                                                                                                                                                                 Department of Genetics, Park Avenue, St. Louis,
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                                                                                                                       Sequencing Center
                                                                                                                                                                 s, Washington
s, Missouri 63108, USA
gi:9838323.
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Missouri 6
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu and

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanase, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc., (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone RP11-708P17 shows evidence of possibly several transposons in the growth of the clone, which is not par part of the

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FEATURES
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mol_type="genomic DNA"

db_xref="taxon:9606"
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1 Similarity 80.0%;
16; Conservative
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Homo sapiens chromosome 19 clone CTD-2050I18, complete sequence.
AC008794
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                              Direct Submission
Submitted (28-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 131972)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                     2 (bases 1 to 131972)
DOB Joint Genome Institute.
Direct Submission
                                                                     Submitted (03-OCT-2001) DOB Joint Genome Institute, 2800 Drive, Walnut Creek, CA 94598, USA on Oct 3, 2001 this sequence version replaced g1:9558576. Draft Sequence Produced by DOB Joint Genome Institute
                                                                                                                                                                                                                          Submitted (03-AUG-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 3 (bases 1 to 131972)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                Unpublished
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DOB Joint Genome Institute and Stanford Human Genome Center.
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            Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.5% of Sequence;
                                                                                                                                     Direct Submission
                                                           www.jgi.doe.gov
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7720._.7776
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13772. .13792
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13465. .13771
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Pred. No. 1.8e+03;
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102831
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                                                                                                                                                                                                                                                                                                                                                         Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., C., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., MacChand, P., Major, J., Matning, J., Mathhaws, C., McCarthy, M., MacGonald, P., Major, J., Manning, J., Mathhas, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubba, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barria, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y. Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira B. Pétron J. W.
                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 132063)
Birren,B., Nusbaum,C. and Lander,B.
Mus musculus chromosome 1, clone RP23-79H24
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="19"
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                Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute,
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147815 bp DNA linear PRI 18-N Human DNA gequence from clone RP5-998H6 on chromosome 20q13 Contains the CDH22 gene for cadherin-like 22, a novel gene CpG islands, complete sequence.
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17; Conserv
                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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HTG; C20orf25; cadherin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Comnor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Piarre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wilson, B., Wilson, B., Wilson, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wilson, B., Wilson, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wilson, B., Wilson, D., Young, G., Zainoun, J., Zembek, L., Viel, R., Wilson, B., Wilson, 
                                              Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGGACAGCCAGGACTACAA 28006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGUACAGCCAGGACUACGA 20
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1 132063: contig of 132063 bp in length.
(bases 1 to 147815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Broad Institute of MIT and Harvard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP23-79H24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                      cadherin; CDH22; CpG island; D20S17; PB-Cadherin.
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Pred. No. 1.8e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
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                                                                                                                                                                                                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                polyA_site
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Clone requests: clonerequest@sanger.ac.uk
On Mar 16, 2001 this sequence version replaced gi:10198608.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
nttp://www.sanger.ac.uk/HGP/Chr20
nps-998H6 is from the library RPCI-5 constructed by the group of
pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Clone left end: RP5-998H6"

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27368. 27489,39965. 40101,50849. 51102,53537. 53730,
27368. 57358,68050. 68169,81505. 81799,91582. 92237))
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27368. .57535,68050. .68169,81505. .81799,91582. .9
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/note="match: EST8: AL732210.1 BG743820.1 BI392191.1
BM943978.1 BQ086149.1 BQ12264.1 BU150580.1
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                                                                                                                                                                                                                                                                                                                                                          complement (14281)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (14275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                match: cDNAs: AB019618.1 AF035300.1 D83348.1"
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RESULT 37
AC164137
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                AC164137
AC164137.2 GI:68299844
HTG; HTGS_PHASE1; HTGS_DRAPT; HTGS_FULLTOP
Pecora; Bovidae; Bovinae; Bos.

(bases 1 to 149208)

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Muzny, D. Marie., Metzker, M. Lee., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Allen, C., Alsbrooks, S., Amin, A., Anguiano, D.,
Angalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, P.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC164137 DNA linear HTG 01-JUL-20
Bos taurus clone CH240-14909, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (cow)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: ESTs: BG717973.1 match: cDNAs: BC031232.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Clone_right_end: RP5-998H6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="RP5-998H6.3-002"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16.8; DB 8;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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VERSION KEYWORDS

ACCESSION

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SOURCE

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Shetty, J., Shvartsbeyn, A., Signey, A., Sorelle, R., Sosa, J., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steinle, M., Strong, R., Sutton, A., Tingey, A., Trejos, Z., Usmani, K., Taylor, T., Walker, B., Wang, J., Walker, B., Wang, J., Walker, B., Wang, J., Walker, B., Wang, J., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Thang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Yon, Shang, J., Zhou, J., Zhou, X., Zhao, S., Smith, H.O.,
                                                                                                                                                            and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..... Zhang,J., Zhou,J., Zhou,X., Zhao,S., Yen,J., Yoon,V., Yoon,V., Zhou,A., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A. Smith,D.R., Holt,R.A., Smith,H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jun 29, 2005 this sequence version replaced gi:67906226. The sequence in this assembly is a combination of BAC based
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Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Bgan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center,
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M., Cree,A., D'Souza,
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RESULT 38
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center: Baylor College of Medicine

AC148601

160241 bp

DNA

linear

HTG 17-MAY-2005

TITLE JOURNAL REFERENCE

AUTHORS TITLE

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Query Match
Best Local Similarity
                                        1 AGGUACAGCCAGGACUACGA 20
AGCTACAGCCTGGACTACGA 20672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Atlas 3.0;
Consensus quality: 145336 bases at least Q40
Consensus quality: 146024 bases at least Q30
Consensus quality: 146570 bases at least Q20
Estimated insert size: 147769; sum-of-contigu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: FIJF Center clone name: CH240-14909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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24156
54518
54568
                                                                                         Conservative
                                                                                                                                                                                               estimated_length=unknown
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                                                                                                          84.0%;
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54517:
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24155: gap of 447 bp
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Pred. No. 1
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                                                                                         Mismatches
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KEYWORDS
SOURCE
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AUTHORS
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Query Match
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**This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

** 14139 14238: gap of unknown length 14239 30771: contig of 14138 bp in length 105981 105980: contig of 1533 bp in length 105981 contig of 175109 bp in length 105981 106080: gap of unknown length 119782 119881: gap of unknown length 119782 119881: gap of unknown length 119782 119881: gap of unknown length 119784 132445 gap of unknown length 119784 13245: gap of unknown length 119784 13245:
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Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gasterosteus aculeatus clone ch213-199b3, WORKING DRAFT SEQUENCE, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-MAR-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gasterosteidae; Gasterosteus.

1 (bases 1 to 160241)
Qin,B., Lih,S., Postlethwait,J. and Roe,B.A.
Gasterosteus aculeatus BAC Clone ch213-199b3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-MAY-2005) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
ON May 17, 2005 this sequence version replaced gi:62734771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OK 73019, USA

3 (bases 1 to 160241)

Qin,B., Lin,S., Postlethwait,J. and Roe,B.A.

Direct Submission
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Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gasterosteus aculeatus"
/mol_type="genomic DNA"
/db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                   /estimated_length=unknown
                                                                                                                                                                                                                                                                       estimated_
                                                                                                                                                                                                                                                                                                                                                                              clone lib="Gasterosteus aculeatus BAC library chori-213"
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      84.0%;
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                                                                                                                                                                                                                length=unknown
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      Score 16.8;
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      14;
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JOURNAL
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AUTHORS
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AC104460/c
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ORGANISM
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Best Local Similarity 80.0 Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-DBC-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 162514)
3 (bases 1 to 162514)
3 (kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Phelps,K.A., Buckley,D., Raymond,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 162514)
Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A.,
Saenphimmachak, C., Phelps, K.A., Buckley, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 1 clone RP11-438011, complete sequence.
AC104460 AL358195
AC104460.2 GI:20336796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-APR-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA on Apr 29, 2002 this sequence version replaced gi:17488642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                Overlapping Sequences:
5': RP11-35L17 AL356361
3': RP11-343J24 AL513543,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haugen, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; 44% of reads Sequencing vector: plasmid; 108752; 56% of reads Chemistry: Dye-terminator ET; 50% of reads Chemistry: Dye-terminator Big Dye; 50% of reads Chemistry: Dye-terminator Big Dye; 50% of reads Assembly program: Phrap; veraion 0.990319 Consensus quality: 162405 bases at least Q40 Consensus quality: 162506 bases at least Q20 Consensus quality: 162514 bases at least Q20 Insert size: 162514; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: University of Washington Genome Center Center Code: UMGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: chr-1
Center clone name: RP11-438011 (sc0707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 8.5x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- Summary Statistics
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BGILI ECORI

	5419	5345	12466	. 12695	6524	6365
	9903	1	8816	8795	8270	8285
	2442	:	3231	;	<800	670
• •	1637	1641	1149	1155	<800	536
	1637		5078	512	<800	293
	5197	5093	4745	4834	1514	
-	5729	5693	14645	1445	<800	9
	1045	1050	3231		1598	1589
	1637	1678	3756	3825	<800	276
<u>.</u>	1737	1767	<800		7866	7722
	<800		6366	1	12069	12481
-	<800	271	4315	4349	2060	2028
	<800	171	2423		2060	2061
	<800	:	1149	•	884	1
	2112	2100	3756	:	1598	1603
	3589	!	<800	!	5595	5607
····	1868	:	8816	;	3680	1
· .	9409	9249	4888	4919	884	876
	<800	171	1042		4307	4298
	7139		6719	;	10477	10527
· .	<800		3041	1	884	864
	<800	512	<800	456	10477	10775
	6531	6382	<800	6	2060	2067
	955	967	8816	8696	2818	2811
						1
	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap	FngrPrnt	SeqDerMap
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84.0%; 80.0%; tive									^800		6035	10477	2524	1386	22201	2978	0	4449	<800	1598	1243	2060	2177	6218	<800	4079	2177	<800	2687	<800	884	<800	884	6524
Score 16.8; DB 8 Pred. No. 1.7e+03 2; Mismatches						,•									3167			24	7176	2	189	132	3192	1307	ĺω	1	2291	5753	230	4646	2590	1711	4023	
DB 8; 9+03; 2;															3231	946		^800	7237	2561	1886	1286	3231	1286	3756	8816	2296	5664	<800	4520	2778	1670	4005	1042
Length 162514; Indels 0;		5293	5726	2153	200	650	331	3165	1.		966	649			869	,00/	1	939	12783		5	1119	444	708	779	:	:	4094	571	3601	20	11	1933	7113
Gaps 0	1116	5419	.5729	2178	<800	<800	. <800	. 3222	. 4800		1045	. <800	4100	2178	955	651/		955	12802	: 8977	5419	1116	~800	. <800	872	<800	5419	4100	<800	3589	<800	<800	1921	7139

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KEYWORDS
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AC073317/c
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; 36*
Sequencing vector: plasmid; 36*
Chemistry: Dye-terminator Big Dye; 36* of reads
Chemistry: Dye-terminator Big Dye; 36* of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149699 bases at least Q40
Consensus quality: 153330 bases at least Q30
Consensus quality: 153040 bases at least Q20
Insert size: 168; agarose-fp
Insert size: 161702; sum-of-contigs
Quality coverage: 4.94 in Q20 bases; agarose-fp
Quality coverage: 5.26 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162701 bp DNA linear HTG 17-NOV-2000
Homo sapiens chromosome UNK clone RP11-195N21, WORKING DRAFT
SEQUENCE, 23 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 162701)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: H NH0195N21
----- Summary Statistics
Sequencing vector: M13; 60%
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63108, USA
Nov 3, 2000 this sequence version replaced gi:10337669
 9791
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contig of 1746 bp in length
contig of 1746 bp in length
gap of unknown length
contig of 2264 bp in length
gap of unknown length
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of 3473
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chromosome=""""
      /note="assembly_name:Contig35
clone_end:T7
vector_side:right"
                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          313. .5058
/note="assembly_name:Contig27"
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|mol_type="genomic DNA"
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                                                                                                               20854. .24320
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13395. .16584
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91569: contig of 7100 bp in length
10169: gap of unknown length
101447: contig of 9778 bp in length
101547: gap of unknown length
119545: contig of 17998 bp in length
119645: gap of unknown length
137645: gap of unknown length
137745: gap of unknown length
137745: gap of unknown length
137745: gap of unknown length
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                                                                                   Homo sapiens chromosome, AC015723
        Homo sapiens (human)
                                                          AC015723.8 GI:13357369
                                                                                                                                        AC015723
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37646. .137745
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                                                                                                         163386 bp DNA linear PRI 01-APR-
ne , clone RP11-168G16, complete sequence.
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                           repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2001 this sequence version replaced gi:13194369. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 163386) Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rerreira, P., PitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                      Center project name: L1410
Center clone name: 168_G_1
                                                                                                                                                                                                                                                                                                               Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                Web
                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
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Tesfaye, S.,

Anderson, S.,

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complement (5059.

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ement(6240
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127341 AGGTACAGCCAGGACTGAGA 127322
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166703 bp DNA linear PRI 18-MAY-200:
Human DNA sequence from clone RP11-271B5 on chromosome 13 Contains
the FGP9 gene for fibroblast growth factor 9 (glia-activating
factor (GAF, HBFG-9)), a ribosomal protein S7 (40S ribosomal
protein S7) (RPS7) pseudogene and two CpG islands, complete
                                 Homo sapiens
                                                              ALI39378
ALI39378.15 GI:8247510
HTG; CpG island; FGF9; GAF; HBFG-9; RPS7.
                                                                                                                                                                                                                                                                                                                                            Similarity 80.0
16; Conservative
Bukaryola; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                  Homo sapiens (human)
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complement (33384 . .39408)
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complement (40516. .42349)
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complement(39417. .39642)
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                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                             Score 16.8; DB 8;
Pred. No. 1.7e+03;
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(glia-activating

.83975)

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                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP11-271B5 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/c elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cambridgeshire, CB10 ISA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 4, 2000 this sequence version replaced gi:8246895.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chr13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: vega@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-MAY-2005) Wellcome Trust Sanger Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo
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                                                                                    AA632627 AA675049 AA884919 AA946776 AA989402 A1078616
A1221350 A1222703 A1334161 A1414273 A1650278 A1795502
A1798776 A1869879 A1953761 A1963033 AL559064 AL583692
AV326729 AW046863 AW236112 AW242338 AW466928 BB2236699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Clone left end: RP11-271B5"
complement(10953. ..11555)
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/note="match: proteins: AAH02014 AAH02866 P02362 P23821
P48155 P50894 Q10101 Q29190 Q90YR7 Q962S0 Q967R2 Q9H1S9
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/db_xref="PSEUDO:CAC17691.1"
/db_xref="UniProt/TrEMBL:Q9H189"
join(53571. .54729,63582. .63685,83730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29ZNS1 "
                                                                                                                                                                                                                                 product="fibroblast growth factor 9 (glia-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pseudo
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oin(53571. .54729,63582. .63685,83730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="RP11-271B5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:9606"
chromosome="13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mplement (10953.
                                                                                                                                                                                       e="match:
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                                                                                                                                                                                                                                                                 _tag="RP11-271B5.2-001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _lib="RPCI-11.1"
                                                                                                                                                                                  ESTB: AA093777 AA253941 AA444271 AA563216
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          112 AW242338 /
796 BE111855 /
050 BF472339 /
178 BM285824 /
                                                               BE668924
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                                                    polyA_site
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                                                                                                                                37013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               locus tag="RP11-271B5.2-003" note="Clone left_end: RP11-282A24" 4005. .84010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="match: ESTs: BI827161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .uocus_tag="RP11-271B5.2-003"
oin(63633..63793,83730..84372)
gene="PGP9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDKVPELYKDILSQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPRGPAVTDLDHLKGILRRRQLYCRTGPHLBIFPNGTIQGTRKDHSRFGILBFISIAV
3LVSIRGVDSGLYLGMNEKGBLYGSEKLTQBCVFRBQFBENWYNTYSSNLYKHVDTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM720010 BM724935 BM926135 BQ084891 BQ085010 BQ343403
                            gene="FGF9"
                                                                                                         gene="FGF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="CAC17692.1"
|db_xref="GI:11544937"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="RP11-271B5.2-002" oin(56542. .56752.63582. .63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="InterPro: IPR002209"
locus_tag="RP11-271B5.2-001"
                                                                                                                              locus_tag="RP11-271B5.2-001"
7013. .87018
                                                                                                                                                                                  jene="FGF9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Clone_right_end: RP11-110K8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="RP11-271B5.2-003"
product="fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin (56542.
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translation="MAPLGEVGNYPGVQDAVPFGNVPVLPVDSPVLLSDHLGQSBAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard_name="OTTHUMP00000018804"
                                                                    ocus_tag="RP11-271B5.2-001"
                                                                                                                                                                                                                                                            jene="FGF9
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478...86483
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|552._.84557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="FGF9"
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pin(63653. .63793,83730. .84372)
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product="fibroblast growth factor 9 (glia-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GOA:P31371"
                                                                                                                                                                                                                                                                                                                                                                          ocus_tag="RP11-271B5.2-001"
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_xref="InterPro:IPR008996"
_xref="UniProt/Swiss-Prot:P31371"
_xref="UniProt/Swiss-Prot:P31371"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t="fibroblast growth factor 9
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AUTHORS
TITLE
JOURNAL
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ORGANISM
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(CE (Dases 1 to 168087)

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(CE (Dases 1) to 168087)

(CE Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., Corum, B.,

Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,

DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,

DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L.,

Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,

Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,

McCarthy, M., Meldrim, J., Mathova, T., Mlenga, V.,

McCarthy, T., Naylor, J., Nguyen, T., Mihova, T., Micol, R.,

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Steolanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,

Direct sinbmission
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Choepel, Y., Collymore, A., Cooke, P., Corum, B., Cardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hilev, I., Chanders, T., Cohnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-MAR-2005) Broad Institute of MIT and Harvard, Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 168087) Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 168087)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166703
/note="Clone_right_end: RP11-271B5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 166703; .7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG 01-JUN-2005
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                                                            ACCESSION
VERSION
                                                                                                                                                                                                                      RESULT 44
AC131061
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                                                                                                                                                          DEFINITION
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                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                       AC131061.3 GI:28913177
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                               pieces
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Submitted (01-JUN-2005) Broad Institute of MIT and Harvard, Charles Street, Cambridge, MA 02141, USA On Jun 1, 2005 this sequence version replaced gi:62629962. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                   1 AGGUACAGCCAGGACUACGA 20
AC131061 187700 bp
Mus musculus clone RP24-115M17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number be preserved.
                                                                                                                                         AGGAACAGCCAGGACTAGGA 42958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L31870
Center clone name: 268_H_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Broad Institute of MIT and Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
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22412
58666
58766
74059
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18697
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    estimated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/
                                                                                                                                                                                                                                                                                                                                                /estimated_length=unknown
                                                                                                                                                                                                                                                                                                                                                                                          estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18596: contig of 18596 bp in length
18696: gap of unknown length
22311: contig of 3615 bp in length
22411: gap of unknown length
58665: contig of 36254 bp in length
58765: gap of unknown length
74058: contig of 15293 bp in length
74158: gap of unknown length
74158: gap of unknown length
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                                                                                                                                                                                                                                                        84.0%;
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                                                                                                                                                                                                                                Score 16.8; DB 14
Pred. No. 1.7e+03;
1; Mismatches 2
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contig of 93929 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length=unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                       length=unknown
    DNA linear HTG 11-MAR-2003
WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                  DB 14; Length 168087;
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REFERENCE

JOURNAL

AUTHORS

REFERENCE

AUTHORS TITLE

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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 11, 2003 this sequence version replaced gi:28394870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 187700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Viel,R., Vo,A., Wilson,B., Wu,X., Wy
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Barna, N., Bastien, V., Bloom, T.,
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                                                                                                                                                                                                                                                                  (bases 1 to 187700)
                                                                                                                   Assembly program: Phrap; version 0.960731
                                                                                                                                                               Sequencing vector: Plasmid, n/a, 100% of reads Chemistry: Dye-terminator Big Dye, 100% of read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Lander, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu, X., Wyman, D., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retta,R., Rise,C., Rogov,P., eaman,S., Severy,P., Smith,C.,
                least Q40
least Q30
                                                                                                                                                                     of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lindblad-Toh, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V., Bloom,T.,
Chang,J., Choepel,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Kamat,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dodge, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
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Insert size: 187000; sum-of-contigs
Quality coverage: 9.4 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 9.4 in Q20 bases; agarose-fp Quality coverage: 9.3 in Q20 bases; sum-of-contigs
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17; Conserv
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Homo sapiens clone RP11-1J10, WORKING DRAFT SEQUENCE, 27 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:6479099.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.center
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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1 (bases 1 to 192104)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1J10
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC011141.3 GI:8072508
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                    Consensus quality: 12774 bases at least Q20
Consensus quality: 18219 bases at least Q20
Consensus quality: 18219 bases at least Q20
Consensus quality: 17930 bases at least Q20
Consensus quality: 17774 bases at least Q20
Consensus quality: 17774 bases at least Q20
Consensus quality: 18219 bases at least Q20
NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L2497 Center clone name: 1_J_10
                                                                                                                                                                                                                       Quality coverage: 3.5 in Q20 bases; Quality coverage: 3.2 in Q20 bases;
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1; Mismatches 2;
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sum-of-contigs
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/mol_type="genomic DNA"
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192104: contig of 22191 bp in length
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69913: gap of 100 bp
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a: contig of 6890 bp in length
a: gap of 100 bp
b: contig of 7222 bp in length
b: gap of 100 bp
c: gap of 7226 bp in length
c: contig of 7226 bp in length
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contig of 2513 bp in
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VERSION KEYWORDS SOURCE

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AGGTACAGCCAGGGCTAGGA 14406
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                                                                                                                             note="assembly_fragment"
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5987. .16086
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6614. .52704
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0894. .46513
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AC135809
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                                                                                                                          MO 63108, USA
On May 28, 2004 this sequence version replaced gi:47084674.
                                                                                                                                                                                     Submitted (29-MAY-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Porest Park Parkway, St.
                                                                                                                                                                                                                                                                          Submitted (28-MAY-2004) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 195041)
                                                                                                                                                                                                                                                                                                                                            Wilson, R.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (08-MAY-2004) Genome Sequencing Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                       Wilson,R.K.
Direct Submission
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Mus musculus BAC clone RP23-353F16 Unpublished (2001)
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Mus musculus BAC clone RP23-353F16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-OCT-2002)
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Center project name: M_BA0353F16
                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                         Contact: submissions@watson.wustl
                                                               Web site: http://genome.wustl.edu
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                     Summary Statistics
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NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be brain genomic DNA. The clone ar obtained from Research Genetics, /www.resgen.com) or

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FEATURES
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This sequence is the entire insert of the clone.
Location/Qualifiers
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545. .660
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/clone lib="RPCI-23"
296. .385
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1349. 1705
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720. .907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="7"
                                                                                                                                                                                                                                                                                      /rpt_family="MaLR" 9710. .9812
                                                                                                                                                                                                                                                                                                             /rpt_family="B4"
8976. .9289
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                                                                                                                                                                                         /rpt_family="Malk"
11628. .11955
                                                                                                                                                                                                                                                                                                                                                          /note="Sequence derived from one plasmid subclone." 8094. .8204
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1622: .2705
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13577. .13937
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2693. .12945
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                         rpt_family="E
16166. .16351
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|5955. .16058
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_family="Alu"
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               family="B2"
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                                  DEFINITION
          ACCESSION
                                                                                                                                                 Query Match 84.0%; Score 16.8; DB 9; Length 195041; Best Local Similarity 85.0%; Pred. No. 1.7e+03; Matches 17; Conservative 1; Mismatches 2; Indels 0;
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                               AC127377 195767 bp DNA linear ROD 01-JAN-2004 Mus musculus BAC clone RP23-51N3 from chromosome 3, complete
          sequence.
AC127377
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23522 . 23672
/rpt_family="Alu"
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16508. .16525
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20649, _2070
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23082 . .23501
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26067. .26211
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28432. .28570
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31586. .31710
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28711. .28810
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5175. .25327
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1. .20462
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                                                                                                      University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Dec 25, 2003 this sequence version replaced gi:38198744.
                                                                                                                                         Submitted (01-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                Direct Submission
Submitted (25-DEC-2003) Genome Sequencing Center, 4444 Forest Park
Parkway. St. Louis, MO 63108, USA
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The sequence of Mus musculus
Unpublished (2001)
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                                                                                                                                                                                                              Parkway, St. Louis, MO (bases 1 to 195767)
                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 195767)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing of Mus musculus Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                        Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                            Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                  mitted (07-NOV-2003)
ckway, St. Louis, MO
(bases 1 to 195767)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 195767)
Center project name: M_BA0051N03
                Contact: submissions@watson.wustl.
                                                                     Center: Washington University Genome Center code: WUGSC
                                                     Web site:
                                                                                                                                                                           Submission
                                                                                                                                                                                                                                                                                                                                                                                                                           (14-JUL-2002) Genome Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:40363333
                                                     http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse)
                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center, 63108, USA
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us BAC clone RP23-51N3
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                                                                                    Sequencing Center
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                                                                                                                                         63108,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality sometiments), an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, se
http://genome.wustl.edu вее

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
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               Unpublished

(Dases 1 to 201745)

(Dases 2 to 201745)

(Dases 3 to 201745)

(Dases 2 to 201745)

(Dases 3 to 201745)

(Dases 4 to 201745)

(Dases 5 to 201745)

(Dases 5 to 201745)

(Dases 6 to 201745)

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17; Conserv
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Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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AC104205
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167203. 163307
/note="CpG island (%GC=73.3,
complement (187130. .187201)
/product="FRNA-Ser"
., Colangelo, M., Collins, S., Coll)
DeArellano, K., Dewar, K., Diaz, J.;
P., Fitzhigh, W., Gage, D., Galagan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SC = -9.21
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Sc=-5.57)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="tRNA-Ser"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Likely pseudogene (HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Likely pseudogene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (house mouse)
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Pred. No. 1
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me 3, clone
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RP23-250M22
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NAL Submitted (26-MAY-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

NCE 4 (bases 1 to 201745)

Anderson, B., Nubbaum, C., Lander, B., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Coke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Erickson, J., Paro, S., Ferreira, P., FitzGerald, M., Gage, D., Brickson, J., Paro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Louin, A., Machin, D., Hagos, B., Hall, J., Horton, L., Lui, A., Mabbitt, R., McCarthy, M., Meldrim, J., Meneus, L., Karatas, A., Kells, C., Landers, T., Commor, T., O'Donnell, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienja, V., McCarthy, M., P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission
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RESUDMITTED (06-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, R. Abouelleil, A., Allen, N., Barren, B., Nusbaum, C., Lander, E., Abouelleil, A., Bastien, V., Bircheson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Charleson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Charleson, M., Collymore, A., Cook, B., Cooke, P., Corum, B., Chaepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Chaepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Chaepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Chang, J., Barders, A., Cooke, P., Corum, B., Chaepel, Y., Collymore, A., Cooke, P., Corum, B., Chang, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Cooke, P., Corum, B., Tilav, I., Linders, A., Cooke, P., Corum, B., Chang, J., Gardyna, G., Graham, J., Grand-Pierre, N., Hafez, N., Hafez, N., Cooke, P., Corum, B., Corum, C., Cooke, P., Corum, B., Corum, C., Corum, B., Corum, C., Cooke, P., Corum, B., Corum, D., Corum, C., Cooke, P., Corum, B., Corum, C., Cooke, P., Corum, B., Corum, C., Corum, C., Cooke, P., Corum, B., Corum, D., Corum, C., Coru
                                                                                            Direct Submission
Submitted (15-JUL-2005) Broad Institute of MIT and Harvard, Submitted (15-JUL-2005) Broad Institute of MIT and Harvard, Charles Street, Cambridge, MA 02141, USA
On Jul 15, 2005 this sequence version replaced gi:66730823.
All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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REFERENCE

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

rpt_family="ORR1D"

JOURNAL

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repeat_region
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----- Project Information
Center project name: L19628
Center clone name: 250_M_22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Broad Institute of MIT and Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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4345 .4422
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19780. .19888
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complement(15589. .15642)
/rpt_family="L2"
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complement (3945.
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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                                                              /rpt_family="Lx2"

complement(27127. .27222)

/rpt_family="Lx2"
                                                                                                                                                                                                                                                        /rpt_family="CT-rich"
23839. .23861
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22016. .22166
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2449. .12514
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    /rpt_family="ORR1D"
28510. .28698
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/rpt_family="B3A"
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7. .26117
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                                              family="(TATG)n"
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KEYWORDS
SOURCE
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VERSION
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AC145989
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Best Local Similarity

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AC145989.1 GI:33386940
HTG: HTGS PHASE1.
Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                              Wilson,R.K.

Direct Submission
Submitted (01-AUG-2003) Genetics, G
Forest Park Parkway, St. Louis, MO
Center project name: C_PT166004
                             Web site:http://
                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                              ACL45989 204393 bp DNA linear HTG 01-AUG-2003
Pan troglodytes chromosome UNK clone RP43-16604, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces
                                                                                                                                                                     The sequence of Pan troglodytes clone 
Unpublished
                                                                                                                                                                                                   Wilson, R.K.
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family="MLT2B1"
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family="B1_MM"
lement (32562. .32690)
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lement(32407.
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                            genome.wustl.edu/gsc/index.shtml
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Pred. No. 1
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                                                                                                  Sequencing Center,
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 FEATURES
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COMMENT

organism="Pan troglodytes"

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Sequencing vector: plasmid; 100% Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.990319 Consensus quality: 189315 bases at least Q40 Consensus quality: 192131 bases at least Q30 Consensus quality: 194979 bases at least Q20
                                                                                                                                                                                                                                                  Sequencing vector: M13; 0%
                                                                                                                                                 of reads
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. of 1302 bp in length unknown length

89404 108293 108393 147660 17374 18706 14591 14691 16089 ocation/Qualifiers contig of 11471 bp in 1 gap of unknown length contig of 14728 bp in 1 gap of unknown length contig of 18889 bp in 1 gap of unknown length gap of unknown length gap of unknown leng contig of 56634 bp gap gap gap c gap o gap c gap o gap o gap of gap o gap o gap o gap cont cont f unknown length g of 9695 bp in 1 f unknown length of 11471 bp in length unknown length of 1515 6109 bp in length length length bp in] length bp in 1 bp in] length bp in length length bp in] bp in length bp in length length length ength ength ength ength length length

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17374. .18705
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13187. .14590
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12029. .13086
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18806. .20080
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                                                  AC158309 206775 bp DNA linear ROD 21-JUL-2
Mus musculus chromosome 3, clone RP23-187N22, complete sequence.
AC158309
 Mus musculus (house mouse)
                                       AC158309.6 GI:71044080
                                                                                                                                               AGGTACAGACAGGACTACCA 167936
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14476. .74575
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AUTHORS
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Substitute (house mouse)

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ISM Mus musculus (house mouse)

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Sciurognathi, Muridae; Mus.

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Bloom, T., Bognslavkiy, L., Boukhgalter, B., Comarata, J., Chang, D.,

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FEATURES BOURCE		TITLE JOURNAL COMMENT		TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
Location/Qualifiers 1. 206775 /organisms "Mus musculus" /mol_type="genomic DNA" /db xref="taxon:10090" /chromosome="3" /map="3"	### ALL repeats were identified using RepeatMasker: Smit, A.P.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, v.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Zimmer, A. and Zody, M. Direct Submission Submitted (21-JUL-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA On Jul 21, 2005 this sequence version replaced gi:66571527.	Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Liu, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrin, J., Meneus, L., Mihova, T., Micoya, V., McCarthy, M., Meldrin, J., Weneus, L., Mihova, T., Malorja, V., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,	hham, L., Grand-Pierre, N., Haft, J., Horton, L., Hulme, W., Il; A., Karatas, A., Kells, C., I. Liu, G., Liu, X., Lui, A., Mabha Hajor, J., Manning, J., Matthew neus, L., Mihova, T., Mlenga, V. n, C., Nguyen, T., Nicol, R., No'Neil, D., Oliver, J., Petters chupka, A., Ramasamy, U., Raym, Roman, J., Schauer, S., Schu, C., Spencer, B., Stange-Thom alamas, J., Tesfaye, S., Theodilley, H., Venkataraman, V.S., man, D., Young, G., Zainoun, J. ad Institute of MIT and Harv MA 02141, USA	ission 10-MAR-2005) Broad Institett eet, Cambridge, MA 02141 to 206775) Nusbaum,C., Lander,E., F. Anderson,S., Arachchi, Anderson,S., Brachchi, Collymore,A., Cook,A., K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P.,
					
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Use of nucleic acids containing unmethylated CPG din the treatment of LPS-associated disorders patent: JP 2001513776-A 28 04-SEP-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION OS Artificial Sequence PN JP 2001513776-A/28

PD 04-SEP-2001

PF 28-FEB-1998 JP 1998537810

PF 28-FEB-1997 US 60/039405

PR 28-FEB-1997 US 60/039405

PC A61K49/00,C07H21/02,C07H21/04,A01N43/04

PC 8ynthetic oligonucleotide FH Key Location/Qualifiers FT Source /organism='Artificial Sequence'
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Krieg, A.M. and Kline, J.N.

Immunostimulatory nucleic acid molecules
Patent: US 6239116-A 60 29-MAY-2001;
Location/Qualifiers
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Method of controlling hematopoiesis
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Method of controlling hematopoiesis by using CpG oligonucleotide
Patent: JP 2002514397-A 60 21-MAY-2002;
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Krieg, A.M. and Weiner, G.
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03-APR-1998 US 60/0807729
ARTHUR M KRIBG,GBORGE WEINER
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JP 2002510644-A/60
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14-MAY-1998 US 60/085516,02-FEB-1999
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                                                                        Unknown
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               1 (bases 1 to 18)
Krieg, A.M. and Hartmann, G.
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mmunostimulatory nucleic acid molecules for activating dendritic
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06-MAY-1998 US 60/084512
ROBERT A GRAMZINSKI,ARTHUR M KRIEG,HEATHER L DAVIS,STEPHEN L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism='Artificial
                                                                                                                                                                                                                                                                                                                                                              organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"
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Pred. No. 4.8e+02
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Patent: US 6429199-A 54 06-AUG-2002;

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AR432481/c
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Sequence 4 from Patent WO0122972.
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1 (bases 1 to 18)

1 (bases 1 to 18)

Krieg,A.M. and Weiher,G.

Method of treating cancer using immunostimulatory oligonucleotides

Patent: US 6653292-A 60 25-NOV-2003;

University of Iowa Research Foundation; Iowa City, IA
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                                                                                                                                             Immunostimulatory nucleic acids Patent: WO 0122972-A 4 05-APR-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION GmbH (DE)
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                                                                            organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
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            100.0%; Score 18; DB 6;
88.9%; Pred. No. 4.8e+02;
cive 2; Mismatches 0
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RESULT 12
AX455590/c
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Sequence 485 from Patent
AX355457
AX355457.1 GI:18620125
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UNIVERSITY OF IOWA RESEARCH POUNDATION (US)
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Immunostimulatory nucleic acids
Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
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llarity 88.9%;
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/mol type="unassigned DNA"
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/note="Synthetic oligonucleotide
phosphorothioate backbone"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Pred. No. 4.8e+02;
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Pred. No. 4.8e+02;
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Patent: WO 0222809-A 67 21-MAR-2002;
Coley Pharmaceutical GmbH (DE)
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other sequences; ar
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Sequence 56 from Patent
AX546917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetic construct synthetic construct
                                                          AX546917.1 GI:25812061
                                                                                                                                                                                                                                                                                                                                                                                                              Inhibition of angiogenesis by nucleic acids Patent: WO 02053141-A 4 11-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bratzler,R.L.
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sequences; artificial sequences.
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                        organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                           note="Synthetic Sequence"
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Patent WO0222809.
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Pred. No. 4.8e+02;
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                                                                                                                                                                                                                                                               18;
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Sequence
AR052611
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                              AR052611.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunostimulatory nucleic acid molecules Patent: JP 2001503267-A 74 13-MAR-2001; UNIVERSITY OF IOWA RESEARCH FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 18)
Krieg, A.M. and Kline, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other sequences; artificial sequences.
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                                                                                                                                                                             AGAGGGUCGCACGCGGUA 18
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ARTHUR M KRIEG,JOEL N KLINE
CCTH21/00,CCTH21/02,CCTH21/04,A61K31/175,A61K31/335,A61K31/47
                                                                                                                                                                                                          Conservative
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JP 2001503267-A/74
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|mol_type="unassigned DNA"
|db_xref="taxon:32630"
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mol_type="genomic DNA"

db_xref="taxon:32630"
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88.9%;
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Pred. No. 4.8e+02;
2; Mismatches 0
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Pred. No. 4.8e+02
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REFERENCE AUTHORS TITLE JOURNAL

FEATURES

ORIGIN

Best Loc Matches

RESULT 14 AX546917/c

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VERSION KEYWORDS SOURCE

ORGANISM

DEFINITION ACCESSION

RESULT 13 AX546865/c

FEATURES

JOURNAL

REFERENCE

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AR630675/c
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BD187524/c
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Unclassified.
1 (bases 1 to 17)
Reed, J.C.
                                                                            AR630675
Sequence 9 from
AR630675
                                                                                                                                                                                                                                                                                                               Reed,
                                 Unknown
                                          Unknown
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                                                                 AR630675.1
                                                                                                                                                                                                                                                                                                                                                                                                                        REGULATION OF bcl-2 GENE EXPRESSION Patent: JP 2003026609-A 9 29-JAN-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct
synthetic construct
other sequences; artificial
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Description of Artificial Sequence: Designed DNA based on
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29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                        19-JUN-2002 JP 2002178753
20-SEP-1993 US 08/124256
                                                                                                                                                                                                                                                       /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="unassigned
                                                                  GI:59766403
                                                                                                                                                                                                 94.4%; Score 17; DB
88.2%; Pred. No. 1.50
Live 2; Mismatches
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SOURCE
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AX513690/c
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Sequence 79 from Patent W00226757.
AX513690
AX513690.1 GI:23559810
                                                                                                                                                                                                                                                         1 AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 289)
Vanbroekhoven,K., Wattiau,P., De mot,R. and Springael,D.
Direct Submission
Submitted (24-DBC-2002) Environmental Technology, Vito (Flemisch Institute for Technological Research), Boeretang 200, Mol 2400,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter sp. S429_2
Acinetobacter sp. S429_2
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
1 (bases 1 to 289)
1 (bases 1 to 289)
1 (vanbroekhoven,K., Wattiau,P., De mot,R. and Springael,D.
Acinetobacter sp. diversity in environmental samples assessed by Acinetobacter 16S rDNA specific PCR-DGGE system
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulation of BCL-2-gene expression
Patent: US 6841541-A 9 11-JAN-2005;
The Trustees of the University of Pennsylvania; Philadelphia,
Location/Qualifiers
1. .17
                                           synthetic construct
synthetic construct
other sequences; artificial sequences.
Kandimalla, B.R., Zhao, Q., Yu, D. and Agrawal, S. Modulation of immunostimulatory activity of immunostimulatory
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                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                     91.1%;
nilarity 83.3%;
Conservative
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<1. .>289
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                                                                                                                                                                                                                                                                                                                                                                  /product="16S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="S429_2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                                                                                                                                                                      Score 16.4; DB 1;
Pred. No. 1.9e+03;
2; Mismatches 1;
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16S
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                              Mus musculus
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HTG; HTGS_PHASEO.
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Mus musculus clone RP23-114F22,
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                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-114F22 Unpublished
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Faro, S., Ferreira, P.,
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Center clone name: 114_F_22
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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Contact: sequence submissions@genome.wi.mit.edu

sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will NOTE: This record contains 78 individual g of 1187 bp in length of 100 bp g of 1203 bp in length of 100 bp of 1166 bp in length 100 bp of 1086 bp in length 1130 bp in bp in bp in length ä ä ä ä length length length length length length length

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Homo sapiens chromosome 17 clone RP11-497H17, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
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On Jun 17, 2000 this sequence version replaced gi:7232172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 88%
Sequencing vector: plasmid; 12%
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Direct Submission
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Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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Quality coverage: 3.98 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                 be preserved
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                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="17"
                                                   /estimated
                                                                              'note="assembly_name:Contig9"
                                                                                                                                       note="assembly_name:Contig8"
                                                                                                                                                                          'estimated
                                                                                                                                                                                                                                                           note="assembly_name:Contig6"
                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig5"
                                                                                                                                                                                                                                                                                                                                                  'clone="RP11-497H17"
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            :e="assembly_name:Contig10"
23. .13022
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g of 6867 bp in 10
f unknown length
g of 5194 bp in 10
f unknown length
g of 10047 bp in
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f unknown length
g of 4624 bp in
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RESULT 25
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                                                                                                                     GAGGGUCGCACGCGGU 17
                                                                                                                                                       Conservative
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13023. .15483
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74424. .79047
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56584. .66683
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37544. .37643
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79048. .79147
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74324. .74423
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31448. .31547
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L8299. .21370
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                                                                                                                                                     Score 16; DB 14;
Pred. No. 9.8e+02;
2; Mismatches 0
544
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 DNA
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 linear
ENV 03-MAY-2004
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AY988985/c
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DEFINITION
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                  137
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Uncultured soil bacterium clone LlA.6F04 16S ribosomal RNA gene,
partial sequence.
AY988985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harris, J.K., Chow, M.L., Chitteranjan, S., Radomski, C.C., McDermott, J.M., Davies, J., Pace, N.R. and Axelrood, P.B. Expansion of the bacterial phylogenetic tree: Significant survey-points for further mapping of bacterial diversity unpublished
     Direct Submission
Submitted (29-MAR-2005) Department of Plant Pathology, University
of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 53705, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-OCT-2001) BC Research
Vancouver, BC V6S 2L2, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular characterization of bacterial diversity in Lodgepole pine (Pinus contorta) rhizosphere soils from British Columbia forest soils differing in disturbance and geographic source FEMS Microbiol Ecol. 42, 347-357 (2002)

2 (bases 1 to 544)

Harris, J.K., Chow, M.L., Chitteranjan, S., Radomski, C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chow, M.L., Radomski, C.C., McDermott, J.M., Davies, J. and Axelrood, P.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uncultured bacterium uncultured bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uncultured bacterium clone S52.30PG 16S ribosomal RNA gene, partial
                                                                                                                                                  Bacteria; environmental samples.
1 (bases 1 to 625)
Schloss, P.D. and Handelsman, J.
                                                                                                                                                                                                         uncultured soil bacterium
                                                                                                                                                                                                                                           ENV
V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chow, M.I., Radomski, C.C., McDermott, J.M., Axelrood, P.E.
                                                                                   2 (bases 1 to 625)
Schloss, P.D. and Handelsman, J.
                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; environmental samples.

1 (bases 1 to 544)
                                                                                                                                     The last word: toward a sample based
                                                                                                                                                                                                                         uncultured soil bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /environmental sample /note="from lodgepole pine rhizosphere soil from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) installation near Prince George, Canada"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="16S ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1. .>544
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/mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="S52.30PG"
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82.4%;
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Pred. No. 5.3e+03;
2; Mismatches 1;
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DQ123747/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2005) Environmental Sciences & Engineering, University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA Location/Qualifiers
                                                             partial sequence
DQ123747
                                                                                               Uncultured soil bacterium
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Singleton, D.R., Sangaiah, R., Gold, A., Ball, L.M. and Aitken, M.D.
Direct Submission
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mol type="genomic DNA"
/isolation_source="pAH-contaminated soil"
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'clone="L1A.6F04"
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'isolation_source="soil"
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clone="PAH-Bio-08"
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                                               GI:71384119
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82.4%;
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82.4%; Pred. No. 4.9e+03;
live 2; Mismatches 1; Indels
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Pred. No. 5.2e+03;
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clone PAH-Bio-87
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somal RNA gene,
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                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (16-AUG-1999) Lukow T., Biogeochemie, Max-Planck-Institut
fuer terrestrische Mikrobiologie, Karl-von-Frisch-Strasse, 35043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16S ribosomal RNA; 16S rRNA gene. rhizosphere soil bacterium RSC-II-71 rhizosphere soil bacterium RSC-II-71
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Rhizosphaerengemeinschaften transgener versus nicht-transgener
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUL-2005) Environmental Sciences & Engineering, University of North Carolina, CB#7431, Chapel Hill, NC 27599, USA
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Singleton, D.R., San
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; environmental samples
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/isolation_source="pAH-contaminated soil"
/db_xref="taxon:164851"
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|mol_type="genomic DNA"
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/product="16S ribosomal RNA"
                                                                                                                                                                            gene="16S rRNA"
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Pred. No. 4.9e+03;
2; Mismatches 1
                                                 Score 15.4; DB 3;
Pred. No. 4.8e+03;
2; Mismatches 1;
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                                                                              Length 1029;
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AY102345
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1 (bases 1 to 1331)

Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C.
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                                                                                                        Submitted (08-MAY-2002) Imperial College at Silwood Park, NERC Center for Population Biology, Ascot, Berks SL5 7PY, UK Location/Qualifiers
                                                                                                                                                                                                                                                          Cultivation-Dependent and -Independent Approaches for Determining Bacterial Diversity in Heavy-Metal-Contaminated Soil Appl. Environ. Microbiol. 69 (6), 3223-3230 (2003)
                                                                                                                                                                                                                                                                                                                                                                                      uncultured bacterium uncultured bacterium
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                                                                                                                                                                        Ellis,R.J., Morgan,P., Weightman,A.J. and Fry,J.C. Direct Submission
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                                                                                                                                                                                                                  (bases 1 to 1331)
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                      /mol_type="genomic DNA"
/db_xref="taxon:77133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:77133"
/clone="a13154"
                                                                organism="uncultured bacterium"
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Pred.
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AUTHORS
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BC082645/c
LOCUS
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ORGANISM
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Best Local S
Matches 14
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                       Klausner, R.D. Collins, F.S., Wagner, L., Shensefer, C.F., Bhat, N.K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, M.B., Bonaldo, M.F., Casawant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Vullalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Villalon, D.K., Muzny, D.M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                              Submitted (15-SEP-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
BC Cancer Agency, info@bcgsc.bc.ca
                                       cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                         NIH-MGC Project
Contact: XGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg, R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein,S.L., Strausberg,R.L., Wagner,L.,
and Richardson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC082645
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                                                                                                      Tissue Procurement: Martha Rebbert, Steven L.
                                                                                                                                                                                          Development, 61
20892-7510, USA
                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                Klein, S. and Gerhard, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Dyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and genomic tools for Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC082645.1 GI:52139140
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                                                                                                                                                                                                                                                                                                                                            12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE: 6864519),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 1871)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feingold, E.A., Grouse, L.H., Derge, J.G.,
                 Vancouver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.4;
Pred. No. 4.
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                      BC, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         research:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pontius, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pipoidea;
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The NIH Xenopus Clifton, S.W

Pipidae;

Klein, Ph.D

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
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BC073203/c
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JOURNAL PUBMED
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Best Local Similarity
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                                                                          BTIIL
                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                          BC073203
Xenopus laevis MC
IMAGE:5156366), «
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
                                                                                                                                                                                                Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peatherstone, Malachi Griffith, Obi Griffith, Ran Guin,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran. I
Dev. Dyn. 225 (4), 384-391 (2002)
12454917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steve Jones,
                                                                  Genetic and genomic tools for Kenopus research: The
                                                                                                  Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.Wand Richardson, P.
                                                                                                                                                Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 2394)
                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                BC073203.1 GI:49255989
                                                initiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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laevis MGC80472 protein, mRNA
156366), complete cds.
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YF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="LOC494668 protein"
/protein_id="AAH82645.1"
/db_xref="GI:52139141"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ?CYRCGKEGHWSKECPLDQMAKELEQEPGYPPESFPDPYGPMRSAAYRTAYAQRVFYD
?GERFSIVDYYQRYRVRPSSYDAILERRVNALPPGASTISYRERIDSPPYERHLLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KAADEAVRNLNHYKLHNVSINVEHSRGKPNASTKLHVSNLSSSCTSEELRAKFEEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="GeneID:494668"
/translation="MVKLFVGNLPPEATQPELKSLFEQFGRVTECDIIKNYGFVHMDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="LOC494668"
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mol_type="mRNA"
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issue type="Embryo, stage 10"
lone lib="NICHD XGC_Emb1"
ab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                xref="GeneID:494668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref="taxon:8355"
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88.2%;
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Pred. No. 4.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                        NA linear VRT 03-
(cDNA clone MGC:80472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1871;
                                                                             NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                  VRT 03-AUG-2004
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AUTHORS
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RS Strausberg, R.L., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villaion, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 153 Row: 1 Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
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Contact: XGC help desk
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20892-7510, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nfo@bcgsc.bc.ca
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                                                                                                        'gene="MGC80472"
                                                                                                                                                                                                                    gene="MGC80472"
                                                                                                                                                                                                                                                                                                                                 (clone="MGC:80472 IMAGE:5156366"
(rissue type="Embryo, stage 10"
(clone lib="NICHD_XGC_Embl"
'lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
product="MGC80472 protein"
|protein_id="AAH73203.1"
                                                                         codon_start=
                                                                                                                                                                                  _xref="GeneID:444116"
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                                                                                                                                                                                                                                                                                          e="Vector: pCMV-SPORT6"
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KEYWORDS
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AC159431
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Best Local
                                                                                                                                   source
                                                                                                                                                                                    Submitted (02-APR-2005) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, nelsayed@tigr.org Medical Center Dr., Rockville, MD 20850, USA, nelsayed@tigr.org Medical Center Dr., Rockville, MD 20850, USA, nelsayed@tigr.org Lockwille, MD 20850, USA, nelsayed@tigr.org Medical Center Dr., Rockville, MD 20850, USA, nelsayed@tigr.org Lockwille, MD 20850, Were done Medical Medical Medical Amountains of algorithm GLIMMER with similarity coordinates) were done manually based on detailed comparisons with the T. cruzi and L. major genomes. Genes on BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. TD03.27F10.410). Gene products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either 'hypothetical protein', or 'hypothetical protein, conserved' in the case of products shwing significant similarity with proteins or domains of unknown function from other organisms. Gene products of unknown function with predicted orthologs in Trypanosoma cruzi and Leishmania major genomes were automatically classified as conserved proteins. Short profein, unilkelv'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ghedin, E., Blandin, G., Bartholomeu, D., Caler, E., Haas, B., Hannick, L., Shallom, J., Hou, L., Djikeng, A., Feldblyum, T., Houteler, J., Johnson, J., Johnson, J., Kalak, H., Larkin, C., Pai, G., Peterson, J., Khalak, H.G., Salzberg, S., Simpson, A.J., Tallon, L., Van Aken, S., Wanless, D., White, O., Wortman, J., Fraser, C.M. and El-Sayed, N.M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Haas,B., Blandin,G. and El-Sayed,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma brucei chromosome 8 clone RPCI93-28F14, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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DRERFSIIDYYQRYRVRPSSYDTILERRLTGLPPAATVSYREXIESFPYERHLLPPP
PQLPSSYYARERSPIRRSSSASSMEIYRTERRLSPIMENPFADDPRCPRDSYYDRVQ
YL"
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RKAADEAVHNLNQYKLHNVAINVEHSRGKPKASTKLHVSNLSSSCTSDELRAKFEEYG
AVLECDIVKDYAFVHWERSABALDAIKNLENTEFKGKKMHVQLSTSRLEVTPGWGDRT
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/isolate="GUTat10.1"
                                                                                                                                                   Location/Qualifiers
                  /db_xref="taxon:5691"
/chromosome="8"
/clone="RPCI93-28F14"
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overlapping clone 26A17."
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/product="RNA-binding pro
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/note="synonym: Tb08.28F14.40;
                  note="microsatellite"
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COMMENT

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NLTELKAALRECDVDEDGAVRLNDFRSVLSS"
                                                            /translation="MGCLPPDDLGPFVSDHVDVNEAEPVPLSDEDLDLLVRYSLLPTD
VVREAWAVFNHYRVVECLRAQQRHYAMTGHLPQKSTVSMSARPFPVAECGGKLFTTPV
RAASGDCNAVKEEEKAPVSPRDCVTGENSECRKEEVEVAVLGAEGLRQFFEDTGAPIP
              KNFTADVRESEINTLFRTLDVDGDGVVSVDDIQRLLBERCSLGDTLYEDRDIRYLRGM
                              ILEVTSFLREMSQPPVEYLLYQRALEEKLTGAAAAAAPPREESPGVGQRKKSPQTDQS
KHNKGQSVGRGQRPNNNTKSLNILVDDHIDLLEEQRGSGGETVTFPLFLYILSNAELG
                                                                                                        product="hypothetical protein, conserved"
protein_id="AAX70127.1"
db_xref="GI:62176005"
                                                                                                                                                                                                                                  17113. .>18210
locus tag="Tb927.8.2800"
note="synonym: Tb08.28F14.140; hypothetical protein,
conserved".....
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                                                                                                                                                                                                                 locus_tag="Tb927.8.2800"
product="hypothetical protein,
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                                                                                                                                                                                                                                                                                                                                           locus_tag="Tb927.8.2790"
note="synonym: Tb08.28F14.130; acetyl-CoA synthetase
pseudogene), putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="microsatellite"
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AUTHORS
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sequence.
AC159420
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Submitted (02-APR-2005) The Institute for Genomic Research, 971
Submitted (02-APR-2005) The Institute for Genomic Research, 971
Medical Center Dr, Rockville, MD 20850, USA, nelsayed@tigr.org
Medical Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative protein coding regions (>30 codons) were predicted by combining the output of the gene finding along the GIMMER with similarity data and manual annotation of open reading frames. Further refinement of gene models (additions, deletions and alterations to boundary coordinates) were done manually based on detailed comparisons with the T. cruzi and L. major genomes. Genes on BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. Tb03.27F10.410). Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghedin, B., Blandin, G., Bartholomeu, D., Caler, B., Haas, B., Hannick, L., Shallom, J., Hou, L., Djikeng, A., Feldblyum, T., Hostetler, J., Johnson, J., Jones, K., Koo, H.L., Larkin, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, unlikely'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomes were automatically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either 'hypothetical protein', or 'hypothetical protein, conserved' in the case of products showing significant similarity with proteins or domains of unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aken,S., wanies
El-Sayed,N.M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted coding sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               idditional evidence of coding potential were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rypanosoma.
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nilarity 82.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: Tb08.28F14.150; 5'-3' exonuclease XRNC, putative"
                                                                                                                                                                                                    /note="annotation for this sequence region can be
overlapping clone 26N11."
/locus_tag="Tb927.8.2250"
/note="synonym: Tb08.26A17.20; hypothetical protein,
conserved"
                                                                                                                                                                                                                                                                                                                                                clone="RPCI93-26A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nol_type="genomic DNA"
solate="GUTat10.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142479 bp
romosome 8
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Pred. No. 2.1e+03;
2; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      classified as conserved proteins.
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PHITJATAPGYPAKYSNELLSKVSTETSDIKVMEVSPDVSISGVFQFVR*
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conserved"
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DEGLFBKLKBLBGTSIBLKPTHIVMNEKVAAIGVCNNDBFPCQDAHPHILVATAPDAT
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conserved"
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                                                                                                                                                                                                                                                                                                                        QEDIDDVTKKGKIKIFCARKLPDLPPDITIPGEFRFMHW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="Tb927.8.2260"
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                                                                                                                                                  6194. .>8793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="Tb927.8.2270"
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                                              ocus_tag="Tb927.8.2280"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="microsatellite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="microsatellite"
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                            Mismatches
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go_function: ATPase activity [goid 0016887];
go_process: vacuolar acidification [goid 0007035]*
/codon_start=1
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ypvpniaaphyfrrvldahhltnnfdkvlcedgrlpfqagtalarrhevfkrllpfls
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mimfhinanrhilopptknrrgevvsQtqrnrvcpaairayrfl
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DEGLFEKLKELEGTSIELKPTHIVMNEKVAAIGVCNNDEFPCQDAHPHILVATAPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPWGVYHLVYMTYRLRTLGYTVESEEELEVVGMKEVMVLGCPMG1TTFWMMYALYRML
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                                                                                                                                                                                                                              note="go component: vacuolar hydrogen-transporting [goid 0000219];
                                                                                                                                                                                                                                                                                     /locus_tag="Tb927.8.2310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="synonym: Tb08.26A17.100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="synonym: Tb08.26A17.80; hypothetical protein,
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                        Score 15.4; DB 2;
Pred. No. 2.1e+03;
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                                                      Length 142479;
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                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-APR-2002) The Institute for Genomic Research, Medical Center Dr., Rockville, MD 20850, USA. On Apr 5, 2002 this sequence version replaced gi:18425288.

* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                          sequence.
AC007862
                                                                                                                                                                                                                                                                                                                      2 GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            El-Sayed, N.M., Kha
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        El-Sayed,N.M., Ghedin,E., Song,J., Larkin,C., Wanless,D., Jones,K Peterson,J., Hou,L., Zhao,H., Mason,T., Militecher,J., Pai,G., Va Aken,S., Utterback,T., Khalak,H.G., Gerard,C., Leech,V., Ullu,E., Melville,S., White,O., Adams,M.D., Donelson,J.E. and Fraser,C.M.
Trypanosoma brucei GUTatl0.1 RPC193-26A17 BAC genomic sequence
                                                                                                                     AC007862 150671 bp DNA linear Trypanosoma brucei chromosome 2 clone RPCI93-10C8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             El-Sayed, N.M., Khalak, H. and Adams, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medical Center Dr, Rockville, MD 20850, USA 3 (bases 1 to 144820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-NOV-2001) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trypanosoma_brucei
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Trypanosoma brucei
                                                AC007862.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC099556.10 GI:20043112
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                     GAGGGTCGGACGCGGTA 137843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the accession number will be preserved.
1 144820: contig of 144820 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 144820)
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                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Trypanosoma brucei"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="RPCI93-26A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       solate="GUTat10.1"
                                                   GI:62358417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .144820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                         85.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                           Score 15.4;
Pred. No. 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144820 bp DNA linear HTG 05-APR-2002 Omosome VIII clone RPCI93-26A17, ***
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 144820;
                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                        complete
                                                                                                                                                  INV 07-APR-2005
                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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AUTHORS
TITLE
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REFERENCE
AUTHORS
TITLE
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AUTHORS
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BAC clone RPC193-10C8 from Trypanosoma brucei chromosome 2.
Putative protein coding regions (-30 codons) were predicted by combining the output of the gene finding algorithm GLIMMER with similarity data and manual annotation of open reading frames.

Purther refinement of gene models (additions, deletions and alterations to boundary coordinates) were denomenable on BACs were assigned a systematic name based on the chromosome and the BACs were assigned a systematic name based on the chromosome and the BAC from which they originated (e.g. Tb03.27F10.410). Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ghedin,E., Blandin,G., Bartholomeu,D., Caler,E., Haas,B., Hannick,L., Shallom,J., Hou,L., Djikeng,A., Feldblyum,T., Hostetler,J., Johnson,J., Jones,K., Koo,H.L., Larkin,C., Peterson,J., Khalak,H.G., Salzberg,S., Simpson,A.J., Tallo Aken,S., Wanless,D., White,O., Wortman,J., Fraser,C.M. and El-Sayed,N.M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products were assigned a putative function when they shared significant similarity with experimentally characterized gene products or when they contained functionally known protein domains. Gene products were labelled either 'hypothetical protein', or 'hypothetical protein, conserved' in the case of products showing significant similarity with proteins or domains of unknown function from other organisms. Gene products of unknown function with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-JUN-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA 3 (bases 1 to 150671)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted orthologs in Trypanosoma cruzi and Leishmania major genomes were automatically classified as conserved proteins. Short predicted coding sequences (less than 150 codons) with no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein, unlikely'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     additional evidence of coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 150671)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="annotation for this sequence region can be found on voverlapping clone 25N14."
complement(<19525. .>22023)
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/note="gynonym: 1008.65; hypothetical protein, conserved"
                                                                                                                        'note="microsatellite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                 rpt_type=tandem
                                                                                                                                                                         note="GA-rich"
                                                                                                                                                                                                                                                                                                                      note="microsatellite"
                                                                                                                                                                                                                                                                                                                                                                                                                       note="microsatellite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="RPCI93-10C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:5691"
                                                                                                                                                                                                                                                                     _unit="taa"
                                                                                                                                                                                                                                                                                                                                                                       _unit="tta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        late="GUTat10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type="genomic DNA"
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                                                                                                                                                                                                     . 7402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brucei"
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S., Simpson,A.J., Tallon,L., Van
man,J., Fraser,C.M. and
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mRNA
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complement (23432...24976)
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complement(<25773. .>26273)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mvkprsqgprrpavkqadnksvgdrsktavtekmkpsrlvggtt
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complement (<22392. ..>22931)
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TTRQCAGAINADHAGLKSSTLQDSYAGAASRTSCPLAAGVSTIVTDDDIGTCGGSTLT
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SGNRGREQPPSSCSAAPLPPTVARLFPASGELTEHPFBGGTCKATNEVTAAPQPQPLL
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VQQGGCKGQREPIHCSERLPADGTTFSLCSTAGERALHENGRGGDTDSSDVGRSADY
SNSKNVHRYHMGEVGDLQCWMGKQREQPRGEVLNGPRLPTDKLEASLHESPNAAAED
TVESLFRTEDGVVSISGTDFCSKEERSMHDVEEAPHSHVSVSATVTPVTPVLGKEVSS
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SVADSQWVDLESAVHRRVRFLGLHGEVTDCTTPNSPKKSSTPSGGRAPPSRNRTRGII
WNDETLMEEPPTARDEGPGEAKGKDGYPAAGPETNKGRLTTNIEHSDGATSGLMSGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLQHVAVLHHIPGLTDPGTETLNLKDFASHIRRQQRNGELSCPHCLSHQNSAADTPFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein,
                               conserved"
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                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                       AC091290/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 38
                                                                                                                                                                                                                          KEYWORDS
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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26280 AGAGGGTCGCCCGCGGT 26296
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AC091290.9 GI:20127973
HTG; HTGS PHASE1; HTGS DRAFT.
Mis musculus (house mouse)
Mis musculus
Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                               AC091290 286178 bp DNA linear HTG 15-MAY-2002 Mus musculus strain C57BL6/J chromosome 7 clone RP23-27G15, WORKING
                                                                                                                                                                                                                                                                                                                                                                DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGGGUCGCACGCGGU 17
                                                                   (bases 1 to 286178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPDSRFOSHHSMQHRQRLFAPLMSRWRTSRRCASRSSYKRSKRLAGGSSAAGDGWNLA
ERLBQLBQIRVTNFBALBERKQHQQNQQSAATGTGDARAEKHKRAFHATGSGSGST
NDDCTAYSPASMSPNVESKRSRTAAEVDLTI TPRVGNQTGRSLRSLFSBFTSSRFTLDN
NIVKRSGKVSSDGERAACESFGELNDVNEYSIVSCOSSNRGTTGBASPDDDRYNDDH
MULLFALGSIEPEDHLPNSGGSCRRSWGSSKGTRSAPHVLLKRTPRSTTLSYHRTTSV
VASLLQKLMYQDSGKISIKLOSHSTLGLADSKELTSPKQNEQCKKGRRRQBAFWKD
RTMALATVSRKVNNSNGAAALFVOACVKTAGRFVASPFKQNEQCKGGRRRGFAFWKD
RTMALATVSRKVNNSNGAAALFVOACVKTAGRFVASTTTISSPTTIVSGAAFTYAA
TPHVEKSTEKHVPRNTPVHERGKDRRRDGCHFSPERGESGTKPSQSLTFALVGQATKVA
GIRLAVSGGCNGNVTTTQSATPMTARPVCGRRYRTTTCSSNFQSSATAGVLATANKR
SSGCFQTTRRRNVAPGGNVAGPSPSSGSGGAAFFQSQATGIGSRTCGKSMQLSVLSCM
SSGCFQTTRRRNVAPGGNVAGPSPSSGSGGAAFFQSQATGIGSRTCGKSMQLSVLSCM
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THARVGSGESDIFPHPSESMDSDIRVEKGRDPSLKGNLASLNRSSPRDTQPLLDDVKA
PSAFPVQIMHRPPTVFNRTLKRNYEDVALSSGGEGSDDFYEDFNDFADDGEGSGDDFG
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LNSQESVTVDGVNTFLTQDTGITVSQYVSAFASNSTSPRLSPVALGALVSATPLVSNR
AASCERAGSQVSVVLSPLSRPLSLALETPSSTCISVRGSSTRSSAPPQHLSRMSNSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="Tb927.2.2590"
/product="hypochetical protein,
complement (32637. .32954)
/locus_tag="Tb927.2.2590"
/codon_start=1
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complement(28686. .31859)
/locus_tag="Tb927.2.2580"
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syrplaamamianiqavaftdsrrsvfqnkktlpsphgrnitpdaastkgralfsdsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (<32637. .>32954)
/locus_tag="Tb927.2.2590"
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pksdagprfhsllehegeepaksgaessamgvepaaatgkrkgtenlldlmegdddss
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/locus_tag="Tb927.2.2580"
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/locus_tag="Tb927.2.2580"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein,
/protein_id="AAX78886.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (<32637. .>32954)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: 10C8.95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="GI:62358422"
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/protein_id="AAX78885.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GI:62358421"
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82.4%;
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                                 Fusina, M.,
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REFERENCE
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JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: AJV
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 276132 at least Q20
*Consensus quality: 273505 at least Q30
*Consensus quality: 270014 at least Q40
*Consensus quality: 270014 at least Q40
*Stimated insert size: agarose-PP - N/A
Quality coverage: agarose-PP - N/A
Quality coverage: 8.3 x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M. Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,B., Perera,A., Shim,C., Thomas,B. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02139, USA
On Apr 10, 2002 this sequence version replaced gi:19909369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-APR-2002) Harvard Partners Center for Genetics and Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Pusina,M., Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E., Percera, A., Shim,C., Thomas,E. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-APR-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perera,A., Shim,C., Thomas,B. and Kucherlapati,R.
High Throughput Mouse Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Harvard Partners Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center Code: HPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will
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unknown length
of 11200 bp in length
unknown length
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                                                                                                             /estimated_length=unknown
221388. .232587
                                                                                                                                                                                                                                                                                                                                          Location
                                                                                       note="assembly_name:Contig89"
                                                                                                                                                 'note="assembly_name:Contig90"
21368. .221387
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chromosome="7"
note="assembly_name:Contig88"
41891. .241910
                                                   estimated_length=unknown
                                                                                                                                                                                                          estimated
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strain="C57BL6/J"
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060. .212079
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8: contig of 852
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g of 891 bp in length
of unknown length
g of 1329 bp in length
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if unknown length
of 303 bp in length
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g of 1566 bp in length
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of 2061 bp in length
unknown length
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unknown length
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unknown length
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of 2259 bp in length
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                                                                                                                                                                                                                                                                                                                                              complete genome.

Bdellovibrio bacteriovorus HD100

Bdellovibrio bacteriovorus HD100

Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
   Schuster, S.C.
Direct Submis
                                                                                                                                                                        Keller,H., Lambert,C., Evans,K.J., Goesmann,A., Meyer,F., Sockett,R.E. and Schuster,S.C.
A predator unmasked: life cycle of Bdellovibrio bacteriovorus
                                                                                                                                                                                                                                                           Rendulic, S., Jagtap, P.,
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                                                                                                                          Science
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      Submission
                                                                                                                 303 (5658), 689-692 (2004)
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271970. .273103
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270930. .271949
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241911. .250226
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clone_end:SP6
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268383...270586
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268363. .268382
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259674. .263360
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256301. .256320
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270587. .270606
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Pred. No. 1.8e+03;
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                                                                                                                                                                                                                                Goesmann, A., l
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                                                                                                                                                                                                                                      , Baar,C., Lanz,C.,
Meyer,F.,
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SVPFALESENAYALNGKXAADFIQKASNYTQBKADTLFLPANFDGLLALLNPAANAPS
VGS IGIFNSDGSAAFPARDGLMYDGKADTLTGKVAGMGSITTSSKIADGAITENKIAN
GAISTSKIVSAALTSAKILDGSIVTAMMADBAITSAKIADGNVTBNVABAJTSAKI
EDGTIVTSDIADAAITSAKILDGSIVTAMMADBAITSAKIADGNVTDAKINSVSGSKV
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FNPSFPVLASATLYGSKLDGALYNQSTRLPFSFSTARALGMREQP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSNVAVAAGAACGGTPHGRVYFSGGTCSSVGIYQCFNGSTLSLGTVSVPSSCDGDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="immediate early hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bdellovibrio bacteriovorus HD100"
/mol_type="genomic DNA"
/strain="HD100 = DSM 50701 = ATCC 15356 = ICPB
MRLSEQICQWAAKDTTIVQADFTLPVRYQGDSEWQPLVSATDICKKRLTYSNFFPNA
                                                                                                                                                                                                                                                                                                                                                                                                               'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="Bd2874"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein_id="CAE80653.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'locus_tag="Bd2873"
020. .2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAE80652.1"
/db_xref="GI:39576488"
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/transl_table=11
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note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag="Bd2874"
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/13787
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SAIVAGQPGLAGNQAGALGNNKLFVPSMLYMEGNELYISSTLGSQIMKLNVDTYDLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRLSARFHSSHYITHYNGSLIVSDYELNILRKIDLTSGVVSTLAGTLGESGSVDGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGYTLGNLGTNR I RNI GID I DNSGNLWI AGNTNGTLSY I SLTAPYEMKAFAAGPMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGR PAANEDQTKATSRFSS PGDIKYHNGALYISDTVNSCIRR FDMNDTVSVIAGWC
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TRDRTPPDVELTSFLSAQNINGGSTQDISWNYSDAHPAANPVSFYYSLNGGTDWTAIA
VDQLNTSPYSWTTGALNSNQLRLKIIGKDSLGNVTEDVSPVSHLIDSLNPVITLNITP
                                                                                                                                                                                                                                                               /translation="mpklfymosssglsrharpkilsenisalieeegllvrpyghat
lpypnlltaeegegvlrdiliypgvctdvksgngslkdtrlftekaihrlgvsvdppi
lbgigphhlieiytgagtgiprslkppevcsysledlycrkwhlygrspedgekles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glimmer/Critica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVGYQDGAGAAAQFTEPIGIGCITGGAHEGVYVNDTRAVRKVTLAGNVTTIAGSLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFGIPAEVTDFRTAGGMPKISSPRFITSDGTNVYLSSANSLRLVHLANQTVTTIAGNS
SLGGITDGPLGTSRFSQPWGVYKVFGGIYSIDRSAATIRFTTNAGVTRTVAGTPNVHG
FIEAASQGDISRFNGPTDLCAIGNSIYLVDNDNARVRRLDVIDINDPVTNPATASIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAVSRAFTRNQLAAKNYDLSFIDPMYRKSGDAVAFDFSSLALDSEVASWKVYFVDDAD
                                                                                                                                                                       9451. .10215
                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAE80656.1"
/db_xref="GI:39576492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /RTFAGTGLTNDGKYVYFTERGSSTVRRLNPATNEVTLWMGNPDFTGHRDGPMPDALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTVARLNQPYGIAVQGNYLYFAERTASLVRAMNLTTNEVFTVMGTANTSGADDGDKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )NDGSYARNIAYARGTNQVKVGDDLYVVSFYDSAVYKVDINGVVSLFAGKPGTPGSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1GGSDGVGTASRFDSLVGMDVVGNTLYLAENTGRLRMMDLDSGTVTSVINKDFATSTF
AGRMMTYVNKSGFYDVVIIGTSAYVTQINLNTLLRISLVNBBIEQMVGYGLIRDNYKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGYTTASAGPGREVSIGHAVGIATDGTYVYFSDHTRHCILRYNPSPMVKTVEVLLGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3QEPVNGNAADGLPGIARLDAPYALTRLGSNLILADRYYIRSIDTTVPAMPIVSTLVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ADLNTSTLVFAARATDKVGR I TDVFSQAFTI DNGS PALTWAS PADGSNG I NGI TASG
ACGSASGDGAVVTLTGD I VGAPVNTACTAGNWSVAVVFNSGFGAKS I TATQSDHAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )HTQAHKGGEVLVFDWLATDANLGPNPVVIAYTVDGTNWIMVNSIASHPSSGTMNVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aslrviltdssgktletesglaidstppvipaitdetpalsretmahftladcsdakf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_t_
_51. .8666
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/locus_tag="Bd2877"
/note="ABC-type amino acid transport/signal transduction
systems, periplasmic component
                                                                                                                                                                                                                                                                                                                                                                    db_xref="UniProt/TrEMBL:Q6MJA5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="putative hemagglutinin/hemolysin-related"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           evidence=not_experimental transl_table=11
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                                                                                                 locus_tag="Bd2877"
451. .10215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="hypothetical protein predicted by
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note="hypothetical protein"
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10te="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [QPHFTPEGMYISSGDHYNVRLAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="UniProt/TrEMBL:Q6MJA6"
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                                                                                                                                                                                                                                   YSQSPMRTLKATAPEHTIRATTSLERNEIITQILWLSPLFSNTKADSYILAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _tag="Bd2876"
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SOURCE
ORGANISM
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BX248356/c
LOCUS
                                                                                                                             REFERENCE
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Best Local
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Corynebacterium diphtheriae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGAGGGUCGCACGCGGU 17
                                      Direct Submission
Submitted (03-OCT-2003) Cerdeno-Tarraga A.M., submitted on behalf of the Pathogen Sequencing Unit, Sanger Institute, Wellcome Trust
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segment 3/8.
BX248356 BX248353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX248356 BCT 17-APR Corynebacterium diphtheriae gravia NCTC13129, complete genome;
                                                                                                                                                                                          Whitehead, S., Barrell, B.G. and The complete genome sequence ar diphtheriae NCTC13129
                                                                                                                                                                                                                                                                                                                 Cerdeno-Tarraga, A.M., Efstratiou, A., Dover, L.G., Holden, M.T., Pallen, M., Bentley, S.D., Besra, G.S., Churcher, C., James, K.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX248356.1 GI:38199583
                                                                                                                                                                                                                                                      Hamlin,N., Holroyd,S., Jagels,K., P
Rabbinowitsch,E., Rutherford,K.M.,
                                                                                                                                                                                                                                                                           Zoysa,A., Chillingworth,T., Cronin,A., Dowd,L., Feltwell,T
Hamlin,N., Holroyd,S., Jagels,K., Moule,S., Quail,M.A.,
Genome Campus, Hinxton,
amct@sanger.ac.uk
                                                                                                         Cerdeno-Tarraga, A.M.
                                                                                                                                                                        Nucleic Acids Res. 31
                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterineae; Corynebacteriaceae; Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                               (bases 1 to 347625)
                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 347625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative membrane protein"
/protein_id="CAE80658.1"
/db_xref="GI:39576494"
/db_xref="GOA:Q6MJA3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYNLESPWYLAERKDH?IEWNKVQDLSKYVAGNVQGVELRPGVKELADQGKLKIETTT
TQNNNILKLATKRVDYIFSDAFVFRYLLATDPKLKKYRNKLQINSKPIVIERYGVALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="UniProt/Trembl:Q6MJA4"
/translation="mavimrmliLalplsantshatskttitlitheappymaealpd
KGAIFFALAKVLKKGGYELNVVFAPSWVRAKMKAQTDPLIDGYAPYRAIENADLFEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein"
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complement (10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="putative ABC-type amino acid transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="InterPro: HNH nuclease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transl_table=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function="Restriction endonuclease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="sp0752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vpotnetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrprasmic protein"
rotein_id="CAE80657.1"
b_xref="GI:39576493"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   odon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocus tag="Bd2878"
inction="Park"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNSAKIIKLINEGSDEFKKHIEDYLRQIEKEKTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tag="sp0752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.4; DB 1;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein"
                                                                                                                                                                        (22), 6516-6523 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                              Parkhill,J.
nd analysis of Corynebacterium
                                                                                                                                                                                                                                                         Thomson, N.R., Unwin, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 344249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative HNH family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCT 17-APR-2005
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FEATURES
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                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                      /locus tag="DIP0720"
/note="1 probable transmembrane helix predicted for
DIP0720 by TMHMM2.0"
                                                                                                                                                                                                                                                                                                                                       /db_xxef="UniProt/Trembl:Q6NIP8"
/tariblation="mtdphassffvrpardyghrayaipvlavitvmvlidvprtpab
/triblation="mtdphassffvrpardyghiaitelpsgefetqkgegtyrtvgna
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Gahackdhckftfvlevergingintaaycgddreamvdatltnpksmthdkrfgfehv
Dagavkdpdlriqlssvdtthglcgnniametscfygichrvvinesrmvrgakfpqq
Dlgayrqylinhevghgigfanhepcgkngelapimmqqtlslsnselfaidanetyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="DIP0718"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (81. .206)
/locus_tag="DIP0718"
/note="Doubtful CDS. No significant database matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus tag="DIP0719"
/note="Similar to Mycobacterium tuberculosis CDC1551
/note="Similar to Mycobacterium tuberculosis CDC1551
hypothetical 10.1 kDa protein MT3304 TR.AAK47646
(EMBL:AE007142) (97 aa) fasta scores: E(): 4.5e-11, 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Signal peptide predicted for DIP0718 by SignalP 2.0 HMM (Signal peptide probability 0.699) with cleavage site probability 0.667 between residues 22 and 23"
                                                                                                      /locus_tag="DIP0720"
/note="ScanRegExp hit to PS00142, Neutral zinc
metallopeptidases, zinc-binding region signature."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="Putative membrane protein"
/protein_id="CAB49242.1"
/db_xref="GI:38199586"
/db_xref="InterPro:IRR006025"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus tag="DIP0720"
/locus tag="DIP0720"
/note="Similar to Mycobacterium tuberculosis hypothetical
31.0 kDa protein Rv3207c or MTCY07D11.19 TR:005859
(EMBL:Z95120) (285 aa) fasta scores: E(): 1.7e-44, 46.69%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Putative membrane protein"
/protein_id="CAB49240.1"
/db_xref="GI.38199584"
                                                                                                                                                                                                                                                                                            535. .603
                                                                                                                                                                                                                                                                                                                    DDGAVCSANPWPYPFA"
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="biotype gravis"
complement(81. .206)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="UniProt/TrEMBL:Q6NIP9"
/translation="MDIKIGPSDSPRELVVSSREDHNEIVDRIHNALRDAEGVLDLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_statt=1
/transT_table=11
/product="Conserved hypothetical
/protein_id="CAB49241.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ld in 72 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MKYRSHNIIVCSLIPPQLPLKARHIPAKIPSSPPVRIVELP"/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="UniProt/TrEMBL:Q6NIQ0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d in 287 aa*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="GI:38199585"
locus_tag="DIP0721
                          ocus_tag="DIP0721"
189. .2246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag="DIP0720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag="DIP0719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               table=11
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/locus_tag="DIP0722" /note="ScanRegExp hit to proteins signature 1."

PS00430,

TonB-dependent receptor

/locus_tag="DIP0723"
/note="Similar to Mycobacterium tuberculosis CDC1551
/note="Similar to Mycobacterium tuberculosis CDC1551
helicase, UvrD/Rep family MT3295 TR:AAK47638
(BMBL:AB007142) (1101 aa) fasta scores: E(): 2.9e-25,

note="ScanRegExp hit to PS00136, Serine proteases, subtilase family, aspartic acid active site."

note="HMMPfam hit to PF00580, UvrD/REP helicase"

locus_tag="DIP0722"
note="HMMPfam hit to PF00580, UvrD/REP helicase"

locus_tag="DIP0722"

'locus_tag="DIP0722"

subtilase 5426. .865 /locus_tag 5426. .865

locus_tag="DIP0723"

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/note="Similar to Mycobacterium leprae hypothetical
protein ML0818 TR.09CG7 (EMBLIALS83919) (287 aa) fasta
scores: E(): 1.2e-34, 39.47% id in 266 aa"
/coden statt=1
/trans[_table=11
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/trans[_table=1]
/trans[_tab
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43.03% id in 1120 aa"

product="Putative helicase"

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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AR052610/c
                                                                                                        RESULT 42
BD187523/c
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KEYWORDS
SOURCE
                                                   DEFINITION
ACCESSION
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Best Local S
Matches 14
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                                                                                                                                                                                   15
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Sequence 8 from patent US
AR052610
             REGULATION OF bc1-2 GENB
BD187523
BD187523.1 GI:32997262
JP 2003026609-A/8.
                                                                                                                                                                                                                                                                                                                                                                                                                         Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 17)
Reed, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AR052610.1
                                                                                         BD187523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Regulation of bcl-2 gene expression Patent: US 5831066-A 8 03-NOV-1998;
                                                                                                                                                                                                                     AGAGGGUCGCACGCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGTCGCACGGGGT 86018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAGGGUCGCACGCGGU 17
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                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKAGKAH I ADFKQVAAEENARLFYVA I TRAEQQVLVTASADPSKKRPVLPYBYLTMLR
NDFPDSVEEWHERGEAEDYVPPAPQEAVFPPNY I VVGAEDVFAAMQKQPDLI SDDDLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPSMDEERSYVADHLAQAYEQHDGDHPFTAAVLVRKRKHSAAIALELQQRGVPVEIVG
LAGLLGIPEVADLVAIATLLVRPYDTQAAMRILAGPSVGLGMADLMALSDRAYNLSGR
DRRATTELSRDPLERLKQIIADTTPSDQDSIVGLAEAVADLDERLDSSDGPRYSAKGS
                                                                                                                                                                                                                                                                                                                                                              organism="unknown"
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Ohvavlhadantyvakastwltnasavpsalrgdakgdedlvgapvfeidtpdtaael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERLRTLAARLRYLRTNSLSNSLPDLFADIERVFGIRTEVLQREDPRSDGATGTAHLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LATKLEAIAPTVSTYDSYAGRLISEYGLLLPVEPSSRLISQTELPQIAHSIVSAHTGA
LATSNSPNTVTSTLISLVSEMDNHMVSPTDIEBESAAFLAAIEDVBATSKRAPSKEVY
KWRDTQVLANELLPLVQULKTHLANHLMTFGEDMSLAARLAAENPQVBASQRNRVQI
IMLDEYQDTGHAQRVLLKSLPAGTAVTAVGDEMQSIYGMRGATAANLERPLTDEGSNG
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/translation="MLSPQELSCALGQKFPFTPQQADVISSPLAPTLVVAGAGAGKTE
!WAARVVWLVASGLVDPDRVLGLTFTKKAAQQLSKKIRDRLEQLAGIDNLADLDPTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="CAE49245.
db_xref="GI:38199589"
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                                                                                                                                                                                                                                                                      93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.6%;
                                                                                                                                                                                                                                                                                                                                               _type="unassigned DNA"
                                                                                                                                                                                                                                                                        Score 15;
Pred. No.
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5831066.
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                                                                                         linear
                                                                                         PAT 17-JUL-2003
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ORGANISM
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KEYWORDS
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TITLE
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JOURNAL
                                 Matches
                                                Query Match
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                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                       Patent: JP 2002510319-A 25 02-APR-2002;
ISIS PHRMACEUTICALS INC
OS Artificial Sequence
PN JP 2002510319-A/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic construct synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD192460.1 GI:33002199 JP 2002510319-A/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                       the alimentary canal
                                                                                                                                                                                                                                                                                                                                                                                      Compositions and methods for the delivery of oligonucleotides via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the alimentary canal.
                                                                                                                                                                                                                                                                                                                                                                                                      Teng,C.L. and Hardee,G
                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   other sequences;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGGUCGCACGCG 15
 AGAGGGUCGCACGCG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 17)
                                                                                                                                                                                    01-JUL-1997 US 08/886829
CHING LEOU TENG GREG HARDEE.
C12Q1/68, A61K9/127, A61K48/00, C07H21/04
Description of Artificial Sequence: Novel Sequence
Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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JP 2003026609-A/8
29-JAN-2003
                                   Conservative
                                                                                                                                                                                                                                                        01-JUL-1998 JP 1999507295
01-JUL-1997 US 08/8868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence: Designed DNA based on bcl-
                                                                                                                                                                                                                                                                                          02-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-2002 JP 2002178753
20-SEP-1993 US 08/124256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                            organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="synthetic construct"
|mol_type="genomic DNA"
|db_xref="taxon:32630"
                                                                                                                                                                             ocation/Qualifiers
                                                  83.3%;
93.3%;
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                                 Score 15; DB
Pred. No. 1.5e
1; Mismatches
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Pred. No. 1.5e+04;
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                                                                 DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 17;
                                                                 Length 17;
                                 0;
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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G22341
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AUTHORS
TITLE
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Bource
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AR653968/c
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AR630674/c
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Matches 14
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Best Local
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                                   G22341

Auman STS WI-11635, sequence to G22341

G22341.1 GI:1342667

STS; STS sequence; primer; sequence to sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
AR653968
                                                                                                                                                                                                                                                                                                            Compositions and methods for the delivery of oligonucleotides via
the alimentary canal
Patent: US 6887906-A 25 03-MAY-2005;
ISISPharmaceuticals, Inc.; Carlsbad, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGAGGGUCGCACGCG 15
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 17)
Teng, C.-L. and Hardee, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulation of BCL-2-gene expression
Patent: US 6841541-A 8 11-JAN-2005;
The Trustees of the University of Pennsylvania; Philadelphia, PA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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AR630674
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                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
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                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                        organism="unknown"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:67584835
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93.3%;
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93.3%;
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                                               primer; sequence tagged
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Pred. No. 1.5e+04;
1; Mismatches 0
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Pred. No. 1.5e+04;
1; Mismatches 0
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d site.
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                                                   site
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                                                                                                  31-MAY-1996
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primer_bind
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AUTHORS
TITLE
                                                                                                             RESULT 47
BD186637
LOCUS
DBFINITION
ACCESSION
VERSION
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ORGANISM
              REFERENCE
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Best Local Similarity
Matches 13; Conserv
 AUTHORS
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                                                                                                                                                                                                                               318
                                                                    Homo sapiens (human)
                                                                                                                           BD186637 77:
Nucleic acids isolated from
BD186637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derived from dbEST (genbank accession R09557).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whitehead Institute/MIT Center for Genome R
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
                                                                                              BD186637.1 GI:31878837
WO 02097093-A/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STS size: 125
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protocol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer A: AAAACGAAACAAAACAAAATGG
Primer B: TCTAGTTCTGCAGCAAGTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mapped STSs
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Nakagawara,A
                                         Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitehead Institute/MIT Center for Genome Research; Physically
             Hominidae; Homo.
1 (bases 1 to 779)
                                                                                                                                                                                                                               AGGGTCGCACGCGGT 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Template: 10 ng
Primer: each 5 pM
dNTPB: each 4 nM
Tag Polymerase: 0.025 units/ul
Total Vol: 20 ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tris-HCL: 10 mM
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KCl: 50 mM
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Annealing: 56 degrees (
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                         complement (122. .143)
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="417.8 cR from top
                                                                                                                                                                                                                                                                                                  83.3%;
86.7%;
                                         Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                    Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                            neuroblastoma
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8.8e+03;
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REFERENCE
AUTHORS
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AX333656
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ORGANISM
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CQ729047
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KEYWORDS
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JOURNAL
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PC C12N15/11,C1
CC nbla-10589-f
FH Key
FT source
                                                                                                                                                34
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                                                                                                                                                               2 GAGGGUCGCACGCGG 16
                                                                                                                                                                                                       14;
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Sequence 14981 from Patent WO02068579.
CQ729047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids isolated from neuroblastoma
Patent: WO 02097093-A 58 05-DEC-2002;
CHIBA PREF, HISAMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAWARA
OS Homo sapiens (human)
PN WO 02097093-A/58
PD 05-DEC-2002
PF 30-MAY-2002 WO 2002JP005294
PF 30-MAY-2001 JP 01P 162775, 24-AUG-2001 JP 01P 255224
                                                                                                                                                                                                                                                                                                                                                                                               Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAGGGUCGCACGCGG 16
                                            AX333656 1936 bp I
Sequence 4165 from Patent WO0194629,
AX333656
                                                                                                                                                                                                                                                                                                                                      Patent: WO 02068579-A 14981 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
Homo sapiens (human)
                              AX333656.1 GI:18124375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQ729047.1 GI:42299514
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Dugas, M., Eils, R., Brofs, B. and Rergent)
Novel genetic markers for leukemias
Patent: WO 03039443-A 2179 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
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933 Mai 7723 Ra 7719 Ra 574 Pol	321 Dro 2722 M. 9751 Ri	5007 Ba	327 DNA	58719 Bacter	2541 Hu	6264 C3 877 Hum	/31 Dro	990 Hum	5876 Hu 8250 Ba	3174 M.	1 56 Pro 7116 Ba	126 Hum	Adj92563 Human DNA Abd09837 Pseudomon	813 Hum	562 CDN	613 Oli	849 Hum	719 Oli 1007 Hu	147 N. 718 Oli	859 Hum 872 Hum	749 Hum	071 MLP	0228 Hu 609 Bac	478 CDN	0229 Human mus	491 Hum 479 cDN	886 Dro	1920 Th	9438 P1	7479 A. margin	918 Lip	4117 Hu	4116 Hu	158 Bcl						2 5
ze nat t gene t gene ynucle	sophil xanth ce abi	ctería	encod	cteria	man DN	5 prom	ant fu	an MTC	man nu cteria	xanth	karyot	an sec	man DN	lan 2P1	A enco	gonuc1	an sig	gonucl	mening gonucl	ian poi	an sec	relat	man mu	cDNA enco	man mu	CDNA enco	sophi1	motic	ant fu	margin	id bio	Human bcl	Human bcl	່ຜ່	2-tar isense	Deletion	get bo	Target bo	Antisense Antisense	cl-2 ant
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	231 13.4 74. 232 13.4 74. 233 13.4 74.	229 13.4 230 13.4	227 13.4 228 13.4	225 13.4 74. 226 13.4 74.	224 13.4	222 13.4 6 223 13.4	220 13.4 221 13.4	C 219 13.4	C 217 13.4 C 218 13.4	C 216 13.4	C 214 13.4	212 13.3	211 13.4	210 13.4	208 13.8	C 206 13.8 C 207 13.8	205 13.8	C 203 13.8	c 201 13.8 c 202 13.8	C 199 13.8 76. C 200 13.8 76.	198 13.8 76.	196 13.8 76.	C 194 13.8 76.	C 193 13.8 76.	191 13.8 76.	C 189 13.8 76.	C 188 13.8 76.	186 13.8 76. 187 13.8 76.	185 13.8 76.	C 183 13.8 76.	C 182 13.8 76.	180 13.8 76.	179 13.8 76.	C 177 13.8 76.	175 13.8 76. 176 13.8 76.	174 13.8 76.	172 13.8 76.	171 13.8 76.	169 13.8	168 13.8 76.
234 13.4 74.4 235 13.4 74.4 236 13.4 74.4 236 13.4 74.4 237 13.4 74.4	231 13.4 74.4 232 13.4 74.4 233 13.4 74.4	229 13.4 74.4 230 13.4 74.4	227 13.4 74.4 228 13.4 74.4	225 13.4 74.4 226 13.4 74.4	224 13.4 74.4	222 13.4 74.4 C 223 13.4 74.4	220 13.4 74.4 221 13.4 74.4	C 219 13.4 74.4	C 217 13.4 74.4 C 218 13.4 74.4	C 216 13.4 74.4	C 214 13.4 74.4	213 13.4 74.4	211 13.4 74.4 212 13.4 74.4	210 13.4 74.4 210 13.4 74.4	208 13.8 76.7	C 206 13.8 76.7 C 207 13.8 76.7	205 13.8 76.7	C 203 13.8 76.7	C 201 13.8 76.7 C 202 13.8 76.7	C 199 13.8 76.7 C 200 13.8 76.7	198 13.8 76.7	196 13.8 76.7	C 194 13.8 76.7	C 193 13.8 76.7	191 13.8 76.7	C 189 13.8 76.7	C 188 13.8 76.7	186 13.8 76.7 187 13.8 76.7	185 13.8 76.7	C 183 13.8 76.7	C 182 13.8 76.7	180 13.8 76.7 2 181 13.8 76.7	179 13.8 76.7	C 177 13.8 76.7	175 13.8 76.7 176 13.8 76.7	174 13.8 76.7	172 13.8 76.7 173 13.8 76.7	171 13.8 76.7	169 13.8 76.7	168 13.8 76.7
234 13.4 74.4 1189 14 235 13.4 74.4 1297 6 236 13.4 74.4 1297 6 237 13.4 74.4 1339 14	231 13.4 74.4 726 14 232 13.4 74.4 822 14 233 13.4 74.4 1176 14	229 13.4 74.4 712 10 230 13.4 74.4 712 10	227 13.4 74.4 627 13 228 13.4 74.4 700 4	225 13.4 74.4 610 6 226 13.4 74.4 610 6	224 13.4 74.4 598 10	222 13.4 74.4 563 3	220 13.4 74.4 496 9 221 13.4 74.4 545 13	C 219 13.4 74.4 471 8	C 217 13.4 74.4 448 14 C 218 13.4 74.4 471 5	C 216 13.4 74.4 442 8	C 214 13.4 74.4 426 8	213 13.4 74.4 382 3	211 13.4 74.4 179 6 212 13.4 74.4 293 6	C 209 13.4 74.4 34 14 210 13.4 74.4 109 2	208 13.8 76.7 347001 12	C 206 13.8 76.7 265118 5	205 13.8 76.7 203654 10	C 203 13.8 76.7 150071 12	C 201 13.8 76.7 149158 12 C 202 13.8 76.7 149261 12	C 199 13.8 76.7 110000 1: C 200 13.8 76.7 112460 6	198 13.8 76.7 110000 1:	196 13.8 76.7 81145 4	C 194 13.8 76.7 53178 8	C 193 13.8 76.7 53178 4	191 13.8 76.7 50000 4	C 189 13.8 76.7 17062 4 C 190 13.8 76.7 25617 9	C 188 13.8 76.7 15782 1	186 13.8 76.7 10557 6 187 13.8 76.7 14180 4	185 13.8 76.7 10016 4	C 183 13.8 76.7 9302 10	C 182 13.8 76.7 9302 6	180 13.8 76.7 8346 6	179 13.8 76.7 6866 6	C 177 13.8 76.7 6855 1:	175 13.8 76.7 6855 6 176 13.8 76.7 6855 8	174 13.8 76.7 6816 12	172 13.8 76.7 6816 6 173 13.8 76.7 6816 8	171 13.8 76.7 6497 4	169 13.8 76.7 3768 14 170 13 8 76 7 5973 4	168 13.8 76.7 3506 13
234 13.4 74.4 1189 14 235 13.4 74.4 1297 6 236 13.4 74.4 1297 6 237 13.4 74.4 1339 14	231 13.4 74.4 726 14 232 13.4 74.4 822 14 233 13.4 74.4 1176 14	229 13.4 74.4 712 10 230 13.4 74.4 712 10	227 13.4 74.4 627 13 228 13.4 74.4 700 4	225 13.4 74.4 610 6 226 13.4 74.4 610 6	224 13.4 74.4 598 10	222 13.4 74.4 563 3	220 13.4 74.4 496 9 221 13.4 74.4 545 13	C 219 13.4 74.4 471 8	C 217 13.4 74.4 448 14 C 218 13.4 74.4 471 5	C 216 13.4 74.4 442 8	C 214 13.4 74.4 426 8	213 13.4 74.4 382 3	211 13.4 74.4 179 6 212 13.4 74.4 293 6	C 209 13.4 74.4 34 14 210 13.4 74.4 109 2	208 13.8 76.7 347001 12	C 206 13.8 76.7 265118 5	205 13.8 76.7 203654 10	C 203 13.8 76.7 150071 12	C 201 13.8 76.7 149158 12 C 202 13.8 76.7 149261 12	C 199 13.8 76.7 110000 1: C 200 13.8 76.7 112460 6	198 13.8 76.7 110000 1:	196 13.8 76.7 81145 4	C 194 13.8 76.7 53178 8	C 193 13.8 76.7 53178 4	191 13.8 76.7 50000 4	C 189 13.8 76.7 17062 4 C 190 13.8 76.7 25617 9	C 188 13.8 76.7 15782 1	186 13.8 76.7 10557 6 187 13.8 76.7 14180 4	185 13.8 76.7 10016 4	C 183 13.8 76.7 9302 10	C 182 13.8 76.7 9302 6	180 13.8 76.7 8346 6	179 13.8 76.7 6866 6	C 177 13.8 76.7 6855 1:	175 13.8 76.7 6855 6 176 13.8 76.7 6855 8	174 13.8 76.7 6816 12	172 13.8 76.7 6816 6 173 13.8 76.7 6816 8	171 13.8 76.7 6497 4	169 13.8 76.7 3768 14 ADX585	168 13.8 76.7 3506 13 ADW507
234 13.4 74.4 1189 235 13.4 74.4 1297 235 13.4 74.4 1297 236 13.4 74.4 1297 237 13.4 74.4 1339	231 13.4 74.4 726 14 232 13.4 74.4 822 14 233 13.4 74.4 1176 14	229 13.4 74.4 712 10 230 13.4 74.4 712 10	227 13.4 74.4 627 13 228 13.4 74.4 700 4	225 13.4 74.4 610 6 226 13.4 74.4 610 6	224 13.4 74.4 598 10	222 13.4 74.4 563 3	220 13.4 74.4 496 9 221 13.4 74.4 545 13	C 219 13.4 74.4 471 8	C 217 13.4 74.4 448 14 C 218 13.4 74.4 471 5	C 216 13.4 74.4 442 8	C 214 13.4 74.4 426 8	213 13.4 74.4 382 3	211 13.4 74.4 179 6 212 13.4 74.4 293 6	C 209 13.4 74.4 34 14 210 13.4 74.4 109 2	208 13.8 76.7 347001 12	C 206 13.8 76.7 265118 5	205 13.8 76.7 203654 10	C 203 13.8 76.7 150071 12	C 201 13.8 76.7 149158 C 202 13.8 76.7 149261	C 199 13.8 76.7 110000 1: C 200 13.8 76.7 112460 6	198 13.8 76.7 110000 1:	196 13.8 76.7 81145 4	C 194 13.8 76.7 53178 8	C 193 13.8 76.7 53178 4	191 13.8 76.7 50000 4	C 189 13.8 76.7 17062 4 C 190 13.8 76.7 25617 9	C 188 13.8 76.7 15782 1	186 13.8 76.7 10557 6 187 13.8 76.7 14180 4	185 13.8 76.7 10016 4	C 183 13.8 76.7 9302 10	C 182 13.8 76.7 9302 6	180 13.8 76.7 8346	179 13.8 76.7 6866 6	C 177 13.8 76.7 6855 1:	175 13.8 76.7 6855 6 176 13.8 76.7 6855 8	174 13.8 76.7 6816	172 13.8 76.7 6816 6 173 13.8 76.7 6816 8	171 13.8 76.7 6497 4	169 13.8 76.7 3768 14 ADX585	168 13.8 76.7 3506 13 ADW507
234 13.4 74.4 1189 14 235 13.4 74.4 1297 6 236 13.4 74.4 1297 6 237 13.4 74.4 1339 14	231 13.4 74.4 726 14 232 13.4 74.4 822 14 233 13.4 74.4 1176 14	229 13.4 74.4 712 10 230 13.4 74.4 712 10	227 13.4 74.4 627 13 228 13.4 74.4 700 4	225 13.4 74.4 610 6 226 13.4 74.4 610 6	224 13.4 74.4 598 10	222 13.4 74.4 563 3	220 13.4 74.4 496 9 221 13.4 74.4 545 13	C 219 13.4 74.4 471 8	C 217 13.4 74.4 448 14 C 218 13.4 74.4 471 5	C 216 13.4 74.4 442 8	C 214 13.4 74.4 426 8	213 13.4 74.4 382 3	211 13.4 74.4 179 6 212 13.4 74.4 293 6	C 209 13.4 74.4 34 14 210 13.4 74.4 109 2	208 13.8 76.7 347001 12	C 206 13.8 76.7 265118 5	205 13.8 76.7 203654 10	C 203 13.8 76.7 150071 12	C 201 13.8 76.7 149158 12 C 202 13.8 76.7 149261 12	C 199 13.8 76.7 110000 1: C 200 13.8 76.7 112460 6	198 13.8 76.7 110000 1:	196 13.8 76.7 81145 4	C 194 13.8 76.7 53178 8	C 193 13.8 76.7 53178 4	191 13.8 76.7 50000 4	C 189 13.8 76.7 17062 4 C 190 13.8 76.7 25617 9	C 188 13.8 76.7 15782 1	186 13.8 76.7 10557 6 187 13.8 76.7 14180 4	185 13.8 76.7 10016 4	C 183 13.8 76.7 9302 10	C 182 13.8 76.7 9302 6	180 13.8 76.7 8346 6	179 13.8 76.7 6866 6	C 177 13.8 76.7 6855 1:	175 13.8 76.7 6855 6 176 13.8 76.7 6855 8	174 13.8 76.7 6816 12	172 13.8 76.7 6816 6 173 13.8 76.7 6816 8	171 13.8 76.7 6497 4	169 13.8 76.7 3768 14 ADX585	168 13.8 76.7 3506 13 ADW507
234 13.4 74.4 1189 14 ACL63669 235 13.4 74.4 1297 6 ABQ32494 236 13.4 74.4 1297 6 ABQ32495 237 13.4 74.4 1339 14 ADW16628	231 13.4 74.4 726 14 ACL6693B 232 13.4 74.4 822 14 ACL678B61 233 13.4 74.4 1176 14 ACL6876	229 13.4 74.4 712 10 ADC72632 230 13.4 74.4 712 10 ADC72639	227 13.4 74.4 627 13 ACM54102 228 13.4 74.4 700 4 AAH93248	225 13.4 74.4 610 6 ABQ50888 226 13.4 74.4 610 6 ABQ50889	224 13.4 74.4 598 10 ADD33179	222 13.4 74.4 563 3 AAC56121	220 13.4 74.4 496 9 ACH45635 221 13.4 74.4 545 13 ADQ51808	C 219 13.4 74.4 471 8 ACA01787	C 217 13.4 74.4 448 14 ABB15166 C 218 13.4 74.4 471 5 AAH68273	C 216 13.4 74.4 442 8 ABX39195	C 214 13.4 74.4 426 8 ABX44832	213 13.4 74.4 382 3 AAC57209	211 13.4 74.4 179 6 ABK30327	C 209 13.4 74.4 34 14 ABROUZY1 210 13.4 74.4 109 2 AAT23338	208 13.8 76.7 347001 12 ADP43517	c 206 13.8 76.7 265118 5 AAH41227 c 207 13.8 76.7 337344 13 ABD32715	205 13.8 76.7 203654 10 ABX16034	C 203 13.8 76.7 150071 12 ADP74216	c 201 13.8 76.7 149158 12 ADP74211 c 202 13.8 76.7 149261 12 ADP74212	C 199 13.8 76.7 110000 11 ADM27081_01 C 200 13.8 76.7 112460 6 ABK83567	198 13.8 76.7 110000 11 ADM27081_01	196 13.8 76.7 81145 4 AAF54868	C 194 13.8 76.7 53178 8 ACF64472	C 193 13.8 76.7 53178 4 AASS9543	191 13.8 76.7 50000 4 ANFS4867	C 189 13.8 76.7 17062 4 ABL14164	C 188 13.8 76.7 15782 14 ACL64631	186 13.8 76.7 10557 6 AAS18240 187 13.8 76.7 14180 4 ABL17324	185 13.8 76.7 10016 4 ABL17322	C 183 13.8 76.7 9302 10 ADC11178	C 182 13.8 76.7 9302 6 ABQ66891	180 13.8 76.7 8346 6 ABK28327	179 13.8 76.7 6866 6 ABL49320	C 177 13.8 76.7 6855 12 ADH69266	175 13.8 76.7 6855 6 AAS16827 176 13.8 76.7 6855 8 ABX93561	174 13.8 76.7 6816 12 ADH69264	172 13.8 76.7 6816 6 AAS16826	171 13.8 76.7 6497 4 ABL29730	169 13.8 76.7 3768 14 ADX58500	168 13.8 76.7 3506 13 ADW50782
234 13.4 74.4 1189 14 ACL63669 235 13.4 74.4 1297 6 ABQ32494 236 13.4 74.4 1297 6 ABQ32495 237 13.4 74.4 1339 14 ADW16628	231 13.4 74.4 726 14 ACL6693B 232 13.4 74.4 822 14 ACL678B61 233 13.4 74.4 1176 14 ACL6876	229 13.4 74.4 712 10 ADC72632 230 13.4 74.4 712 10 ADC72639	227 13.4 74.4 627 13 ACM54102 228 13.4 74.4 700 4 AAH93248	225 13.4 74.4 610 6 ABQ50888 226 13.4 74.4 610 6 ABQ50889	224 13.4 74.4 598 10 ADD33179	222 13.4 74.4 563 3 AAC56121	220 13.4 74.4 496 9 ACH45635 221 13.4 74.4 545 13 ADQ51808	C 219 13.4 74.4 471 8 ACA01787	C 217 13.4 74.4 448 14 ABB15166 C 218 13.4 74.4 471 5 AAH68273	C 216 13.4 74.4 442 8 ABX39195	C 214 13.4 74.4 426 8 ABX44832	213 13.4 74.4 382 3 AAC57209	211 13.4 74.4 179 6 ABK30327	C 209 13.4 74.4 34 14 ABROUZY1 210 13.4 74.4 109 2 AAT23338	208 13.8 76.7 347001 12 ADP43517	c 206 13.8 76.7 265118 5 AAH41227 c 207 13.8 76.7 337344 13 ABD32715	205 13.8 76.7 203654 10 ABX16034	C 203 13.8 76.7 150071 12 ADP74216	c 201 13.8 76.7 149158 12 ADP74211 c 202 13.8 76.7 149261 12 ADP74212	C 199 13.8 76.7 110000 11 ADM27081_01 C 200 13.8 76.7 112460 6 ABK83567	198 13.8 76.7 110000 11 ADM27081_01	196 13.8 76.7 81145 4 AAF54868	C 194 13.8 76.7 53178 8 ACF64472	C 193 13.8 76.7 53178 4 AASS9543	191 13.8 76.7 50000 4 ANFS4867	C 189 13.8 76.7 17062 4 ABL14164	C 188 13.8 76.7 15782 14 ACL64631	186 13.8 76.7 10557 6 AAS18240 187 13.8 76.7 14180 4 ABL17324	185 13.8 76.7 10016 4 ABL17322	C 183 13.8 76.7 9302 10 ADC11178	C 182 13.8 76.7 9302 6 ABQ66891	180 13.8 76.7 8346 6 ABK28327	179 13.8 76.7 6866 6 ABL49320	C 177 13.8 76.7 6855 12 ADH69266	175 13.8 76.7 6855 6 AAS16827 176 13.8 76.7 6855 8 ABX93561	174 13.8 76.7 6816 12 ADH69264	172 13.8 76.7 6816 6 AAS16826	171 13.8 76.7 6497 4 ABL29730	169 13.8 76.7 3768 14 ADX58500 Adx58501	168 13.8 76.7 3506 13 ADMITTED 168 13.8 76.7 3506 13 ADMITTED 17. 18. 18. 18. 18. 18. 18. 18. 18. 18. 18
234 13.4 74.4 1189 14 235 13.4 74.4 1297 6 236 13.4 74.4 1297 6 237 13.4 74.4 1339 14	231 13.4 74.4 726 14 ACL6693B 232 13.4 74.4 822 14 ACL678B61 233 13.4 74.4 1176 14 ACL6876	229 13.4 74.4 712 10 ADC72632 230 13.4 74.4 712 10 ADC72639	227 13.4 74.4 627 13 ACM54102 228 13.4 74.4 700 4 AAH93248	225 13.4 74.4 610 6 ABQ50888 226 13.4 74.4 610 6 ABQ50889	224 13.4 74.4 598 10 ADD33179	222 13.4 74.4 563 3 AAC56121	220 13.4 74.4 496 9 ACH45635 221 13.4 74.4 545 13 ADQ51808	C 219 13.4 74.4 471 8 ACA01787	C 217 13.4 74.4 448 14 C 218 13.4 74.4 471 5	C 216 13.4 74.4 442 8 ABX39195	C 214 13.4 74.4 426 8 ABX44832	213 13.4 74.4 382 3 AAC57209	211 13.4 74.4 179 6 ABK30327	C 209 13.4 74.4 34 14 ABROUZY1 210 13.4 74.4 109 2 AAT23338	208 13.8 76.7 347001 12 ADP43517	c 206 13.8 76.7 265118 5 AAH41227 c 207 13.8 76.7 337344 13 ABD32715	205 13.8 76.7 203654 10 ABX16034	C 203 13.8 76.7 150071 12 ADP74216	C 201 13.8 76.7 149158 12 C 202 13.8 76.7 149261 12	C 199 13.8 76.7 110000 11 ADM27081_01 C 200 13.8 76.7 112460 6 ABK83567	198 13.8 76.7 110000 11 ADM27081_01	196 13.8 76.7 81145 4 AAF54868	C 194 13.8 76.7 53178 8 ACF64472	C 193 13.8 76.7 53178 4 AASS9543	191 13.8 76.7 50000 4 ANFS4867	C 189 13.8 76.7 17062 4 ABL14164	C 188 13.8 76.7 15782 14 ACL64631	186 13.8 76.7 10557 6 AAS18240 187 13.8 76.7 14180 4 ABL17324	185 13.8 76.7 10016 4 ABL17322	C 183 13.8 76.7 9302 10 ADC11178	C 182 13.8 76.7 9302 6 ABQ66891	180 13.8 76.7 8346 6	179 13.8 76.7 6866 6 ABL49320	C 177 13.8 76.7 6855 12 ADH69266	175 13.8 76.7 6855 6 AAS16827 176 13.8 76.7 6855 8 ABX93561	174 13.8 76.7 6816 12	172 13.8 76.7 6816 6 AAS16826	171 13.8 76.7 6497 4 ABL29730	169 13.8 76.7 3768 14 ADX58500 Adx58501	168 13.8 76.7 3506 13 ADW507

Aav82905 Human N-m	13.4 74.4 3998 2 13.4 74.4 3998 2	Aaa95017 Human N-m Abi99174 Human NMD	13.4 74.4 13.4 74.4	
Abx92872 Human N-m	382 13.4 74.4 3935 10	Human	309 13.4 74.4 3155 3 AAZ3870	
Abx98523 Human N-m	380 13.4 74.4 3935 10 381 13.4 74.4 3935 10		307 13.4 74.4 3155 2 AAQ7938	
Acd98333 Human NMD	378 13.4 74.4 3935 8 379 13.4 74.4 3935 9	Human c	305 13.4 74.4 3070 10 ABX9 306 13.4 74.4 3109 6 ABZ35	
Aal47364 Human NMD	377 13.4 74.4 3935 6		304 13.4 74.4 3070 10 ABX985	
Abi99177 Human NMD	375 13.4 74.4 3935 3 376 13.4 74.4 3935 6	'5 Human N	302 13.4 74.4 3070 9 303 13.4 74.4 3070 10	
Aaz38711 Human NMD	374 13.4 74.4 3935 3		301 13.4 74.4 3070 8	
Aaq79388 Human NMD Aav82897 Human N-m	372 13.4 74.4 3935 2 373 13.4 74.4 3935 2	Abi99187 Human NMD	299 13.4 74.4 3070 6	
Ac127178 Rice abio	370 13.4 74.4 3861 11 371 13.4 74.4 3903 11		29/ 13.4 /4.4 30/0 3 298 13.4 74.4 3070 3	
Aca42615 Prokaryot	369 13.4 74.4 3831 8		296 13.4 74.4 3070 2	
Abx9852/ Human N-m	367 13.4 74.4 3794 10 368 13.4 74.4 3794 10	9 Human N	294 13.4 74.4 3007 10 295 13.4 74.4 3070 2	
Aad59669 Human NMD	366 13.4 74.4 3794 10		293 13.4 74.4 3007 10	
Abx77672 Human N-m Acd98337 Human NMD	364 13.4 74.4 3794 8	'Auman N	291 13.4 74.4 3007 9	
Aal47368 Human NMD	363 13.4 74.4 3794 6	Abx77675 Human N-m	290 13.4 74.4 3007 8	
Aaa95024 Human N-m	361 13.4 74.4 3794 3	Abi99184 Human NMD	288 13.4 74.4 3007 6	
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Aag79392 Human NMD	358 13.4 74.4 3794 2 359 13.4 74.4 3794 2	Aav82904 Human N-m	285 13.4 74.4 3007 2	
Abx34706 Human mdd	C 357 13.4 74.4 3750 8	Aag79395 Human NMD	284 13.4 74.4 2916 2 284 13.4 74.4 3007 2	
Abx98529 Human N-m	355 13.4 74.4 3731 10	Abli6825 Drosophil	282 13.4 74.4 2888 4	
Aad59671 Human NWD	353 13.4 /4.4 3/31 9 354 13.4 74.4 3731 10	Ads57060 Bacterial Aag65490 Human NMD	280 13.4 74.4 2763 13 281 13.4 74.4 2835 2	
Abx77674 Human N-m	352 13.4 74.4 3731 8	Aag65489 Human NMD	279 13.4 74.4 2727 2	
AD199183 Human NMD	350 13.4 74.4 3731 6 351 13.4 74.4 3731 6	Acc44326 Gene enco Aaf26114 C. nassat	277 13.4 74.4 2576 8 278 13.4 74.4 2655 5	
Aaa95026 Human N-m	349 13.4 74.4 3731 3	Aad49613 Human cyt	276 13.4 74.4 2576 8	
Aav82903 Human N-m Aaz38717 Human NMD	347 13.4 74.4 3731 2 348 13.4 74.4 3731 3	Aca42750 Prokaryot Adw16799 Pinus rad	274 13.4 74.4 2340 8 275 13.4 74.4 2514 14	
Aaq79394 Human NMD	346 13.4 74.4 3731 2	Aas54358 Pseudomon	273 13.4 74.4 2340 4	
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Adc13590 Pungal Fte
Aah07870 Human rep
Adc136790 Pungal Fte
Aah07870 Human rep
Adc13670 Pungal Fte
Aah07870 Human rep
Adc1670 Pungal Fte
Aah07870 Pungal Fte
Aah07870

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662666614
                                             ADZ49508

AAS85011

ADF53767

ADI18257

ADV69576

ACL67776

ACL67776

ADV15209

ADV15209

ADZ49144
                                                                                      ADI31337
ADS83404
ACA25958
                                                                                                    ADQ99064
ADB48824
AAF21892
ADM46685
ABQ94237
AAL38737
                                                                                                                                    ADQ86772
ADO82260
ABL61976
             ACL73167
ACL27795
ABQ47759
ABQ47758
ABQ47758
AAF18132
ABQ38699
ABQ38698
                                                                                                                  ADR97395
AAI58843
                                                                                                                           AA160629
                                                                                                                                ADF76529
            Aas85011 DNA encod
Adf53767 Alcohol d
Ad118257 Corynebac
Adv69576 Corynebac
Adv69576 Corynebac
Adv69576 Human cDN
Ady15209 DNA encod
Adz49144 Insulin s
Ac179167 Mr. xanthu
Ac127795 Rice abio
Abq47759 Oligonucl
Abq38698 Oligonucl
Abq38699 Oligonucl
Abq38699 Oligonucl
Abq38699 Oligonucl
                                                                                 Adr97395 Human PGL
Aai58843 Human pol
Adg99064 DNA encod
Adb48824 Novel hum
Aaf21892 Human bre
Add31337 Human cDN
Ada83404 Human lym
Aca25958 Prokaryot
Add249508 Insulin s
                                                                                                                              Adg86772 Human tum
Ado82260 Plant ful
Ab161976 Colon ade
Adf76529 Novel hum
                                                                                                                                    Adq86772
Ado82260
Ab161976 C
   Adm46685 DNA encod
Abq94237 FLO11 gen
                                                                                                                     Human pol
5 Human PGL
Corynebac
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ALIGNMENTS

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RESULT 1
AAV52546;

ID AAV52546;

XX
AC AAV52546;

XX
C AAV52546;

XX
DE Unmethylated CpG din
XX
DE Unmethylated CpG din
XX
Unmethylated CpG din
XX
DE Unmet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unmethylated CpG dinucleotide; immune response; bacterial meningitis; natural killer cell activation; NK cell; Th2 response; neonatal sepsis; pulmonary disorder; asthma; environmentally induced airway disease; bacterial infection; endotoxaemia; therapy; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CpG dinucleotide 1761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0039405P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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맑
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                                                                                                                                                                                                This sequence represents an unmethylated CpG dinucleotide, and can be CC used in the method of the invention. The method is for treating a subject having, or at risk of having an acute decrement in air flow, comprising administering a nucleic acid sequence containing at least one CC unmethylated CpG. The nucleic acids containing an unmethylated CpG CC unmethylated CpG. The nucleic acids containing an unmethylated CpG CC to a Thire cells (NK) or redirecting a subject simmune response from a Th2 CC to a Thiresponse by inducing monocytic and other cells to produce Th1 CC cytokines. They can be used to treat pulmonary disorders having an CC immunologic component, such as asthma or environmentally induced alrway CC disease. They can also be used to treat pulmonary disorders with Gram-CC meningitis, neonatel sepsis, cystic fibrosis, inflammatory bowel disease C meningitis, neonatel sepsis, cystic fibrosis, inflammatory bowel disease C and liver cirrhosis, Gram-negative phaeumonia, Gram-negative abdominal CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or CC an inflammatory response to lipopolysaccharide
                                                                                Query Match
Best Local S
Matches 16
                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 35; 65pp; English
18
                                         μ
                                                                                                     Similarity
                              AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                  18
  AGAGGGTCGCACGCGGTA
                                                                                                                                                                  BP; 2 A; 8 C; 4 G; 4 T; 0 U;
                                                                                  Conservative
                                                                                                 100.0%;
                                                              Pred. ...
2: Mismatches
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                                                                                                                         Score 18;
                                                                                                                                                                  0
                                                                                                                           DB
                                                                                                                                                                  Other;
                                                                                                                         2; Length 18;
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                                                                                Gaps
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01-OCT-1998
                                                standard; DNA; 18
(first entry)
                                                ₽P
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Immunostimulatory; oligodeoxyribonucleotide; ODN; unmethylated Cpg dinucleotide; activate; lymphocyte; immune response; Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease; desensitisation therapy; artificial adjuvant; antibody generation; ss.

Immunostimulatory oligodeoxyribonucleotide of the invention

Synthetic WO9818810-A3

RASULT 2
AAV27720 :
AAV27720 :
XX AAV27720 ;
XX DT 01-OCT-19:
XX Immunostin
XX Immuno
XX Immunos
XX I 30-OCT-1996; 30-OCT-1997; 07-MAY-1998 96US-00738652. 97WO-US019791

(IOWA) UNIV IOWA RES 1998-272127/24. Kline JN; POUND

or autoimmune New immunostimulatory nucleic acid molecules - which contain at least one unmethylated CpG dinucleotide, used for treating e.g. tumours, infections disease.

Disclosure; Page 49; 109pp; English

AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides (ODNs) of the invention. The ODNs contain at least one unmethylated CpG dinucleotide, and have the formula: 5' NIXIGGX2N2 3', where at least one nucleotide separates consecutive CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and N2 does not contain a CCGG tetramer

Use of nucleic acids containing an unmethylated CpG - 1 subject having or at risk of having an acute decrement inhibiting an inflammatory response.

t in

treating air flow

OH P

1998-480941/41.

Krieg

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ARZA1906 /c
ID AAZA19
XX AAZA190
XX AAZA190
XX Z4-JAN
XX CCpG oll
KW human
XX I1-12
XX Synthe
XX Synthe
XX I00A
XX I00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ41906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel synergistic combinations of immunostimulatory oligonucleotides immunopotentiating cytokines are useful for stimulating the immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-620169/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human PBMC;
neoplastic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CpG oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion; human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ41906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL-12 secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or more than one CCG or CGG trimer OR 5' NX1X2CGX3X4N 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weiner G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune response; cancer; HIV; bacterial disease; as disorder; jaagsiekte; B cell; NK cell; 88; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0080729P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducing CpG oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
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subject comprising administering to a subject exposed to an antigen, an immunopotentiating cytokine and an immunostimulatory CpG oligonucleotide to induce a synergistic antigen specific immune response. The methods are useful for treating cancer by stimulating an antigen specific immune response against a cancer antigen. The methods can also be used to treat neoplastic disorders in humans, including but not limited to: sarcoma, neoplastic disorders in humans, including but not limited to: sarcoma,

carcinoma, fibroma, Lymphoma, melanoma, and glioma. The methods are also useful

neuroblastoma, retinoblastoma,

The present invention describes a method using CpG containing oligonucleotides (ONs) for regulating immune system remodeling and for regulating haematopoiesis. The method for inducing an antigen-specific immune response comprises: (1) administering an ON having a sequence including at least the formula (I); and (2) exposing the subject to an antigen specific immune response: 5' XIGGX 3' (I), where the ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and X2 = nucleotides. The method can be used using the subject to an antigen-specific immune response: 5' XIGGX 3' (I), where the ON = includes at least 8 nucleotides; C and G = unmethylated, and X1 and X2 = nucleotides. The method can be used.

where the and X1 and

Use of CpG containing oligonucleotides specific immune response.

for, e.g. inducing

an antigen-

English

Sequences AAZ41856-Z41949 are phosphorothioate CpG oligonucleotides which are used in the invention to induce interleukin-12 (IL-12) secretion from human PBMC. The invention comprises stimulating an immune response in a

Example 8;

Page 80; 91pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methods and compositions may also be applied to treat cancer and tumours in non human subjects, e.g. cats and dogs. Neoplasias affecting agricultural livestock may also be treated and include leukaemia, haemangiopericytoma and bovine ocular neoplasia. Chronic, infectious, contagious diseases of sheep and goats caused by the bacterium Corynebacterium pseudotuberculosis, and contagious lung tumour of sheep caused by jaagsiekte may also be treated. CpG oligonucleotides can be useful in activating B cells, NK cells, and antigen presenting cells, such as monocytes and macrophages. CpG oligonucleotides enhance antibody dependent cellular cytotoxicity and can be used as an adjuvant in conjunction with tumour antigens to protect against a tumour challenge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haematopoiesis; regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response; allergic reaction; infectious disease; asthma; thrombocytopaenia; immunohaemolytic disorder; genetic disorder; haemoglobinopathy, kidney failure; chronic inflammatory disorder; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmune remodeling; thrombopoiesis; anaemia; immune system; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methods may also be used to treat allergic diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                 IMMUNOPHARMACEUTICALS
IMMUNOPHARMACEUTICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                      98US-0085516P.
99US-00241653.
                                                                                                                                                                                                                                                                                                                             99WO-IB001285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; D
Pred. No. 10;
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RESULT 5
AAZ47644/c
ID AAZ47644;
XX
AC AAZ47644;
XX
AC AAZ47644;
XX
DT 01-MAR-2000 (first of the continuation of the continuat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           against an antigen such as cells, cell extracts, proteins, polysaccharides, polysaccharides conjugates, lipids, glycolipids, carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and callergens. It can be used in a subject at risk of developing cancer or an allergic reaction. It can also be used for treating an infectious disease, allergic diseases and asthma, as well as thrombocytopaenia which is drug-induced, due to an autoimmune disorder such as idiopathic thrombocytopenic purpura, or resulting from accidental or therapeutic radiation exposure. It can also be used for treating anaemia such as drug cinduced anaemia, immunohaemolytic disorder, genetic disorders such as companied anaemia, indequate production despite adequate iron stores, chronic disease such as kidney failure, and chronic inflammatory disorder such as sheamatoid arthritis, or anaemia cresulting from accidental or therapeutic radiation exposure. AAZ47932 to AAZ48029 represent phosphorothioate CpG oligonucleotides used in the creamplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 16
   The present invention describes a method for treating and preventing parastic infection by administration of unmethylated CpG oligonucleotides. The CpG oligonucleotides are able to stimulate the innate immune system via the activation of immune cells, such as antige presenting cells, natural killer cells and granulocytes. The CpG oligonucleotides and the method can be used to treat and prevent parastic diseases, such as malaria, helminth diseases, tick and mites humans, animals and poultry. The oligonucleotides may be administered in conjunction with parasiticides or other therapeutic compounds after an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IOWA ) UNIV IOWA RES POUND
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CpG oligonucleotide; antigen presenting cell; natural killer
granulocyte; malaria; helminth disease; tick; mite; ss.
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Matches 16
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The present invention describes methods for inducing interleukin 6 (II-6), interferon-gamma (IFN-gamma) or II-12, or for stimulating natural killer cell lytic activity. The methods comprise administering to the subject or exposing a natural killer cell to an immunostimulatory nucleic acid. Also described are: (1) inducing II-6 in a subject comprising administering to the subject to induce II-6 in the subject the immunostimulatory nucleic acid; (2) stimulating natural killer cell lytic activity comprising exposing a natural killer cell to the immunostimulatory nucleic acid to stimulate natural killer cell lytic activity; (3) inducing interferon-gamma in a subject to treat an immune system deficiency comprising administering to the subject to induce
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                                                                                                                                                                                                                                                                                                                                                                                                  Methods for inducing Il-6, interferon-gamma or Il-12, or stimulating natural killer cell lytic activity in a human, comprise administering the subject or exposing a natural killer cell to immunostimulatory nucleic acids.
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                                 immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Bscherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or also useful for preventing cancer, asthma, infectious disease, allergy or
                                                                                                                                                                                                                                                                                     The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory in acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccinating against tumors, infectious using immunostimulatory Py-rich and TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-273485/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieg AM,
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27-SEP-1999; 99US-0156135P.
23-AUG-2000; 2000US-0227436P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 39; 338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infectious disease; allergy; immune deficiency; phosphorothioate;
immune deficiency. The present sequence can also be used to Th1 to a Th1 immune response and to activate immune cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases, allergies and asthma nucleic acids.
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   Note:
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AGAGGGUCGCACGCGGUA 18

Matches Query Match Best Local

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Similarity

100.0%; 88.9%;

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Mismatches

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Gaps

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No.

Score 18;

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Sequence 18

BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

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Matches
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27-SEP-1999;
23-AUG-2000;
                                    response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or is staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Thi immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                              Vaccinating against tumors, infectious diseases, alle using immunostimulatory Py-rich and TG nucleic acids.
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                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infectious
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                                                                                                                                                                                                           present invention relates to a method for stimulating an immune
                                                                                                                                                                                                                                                                                                          2001-273485/28
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16; Conserv
                           sequence may have a phosphorothicate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease;
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; 99US-0156135P.
; 2000US-0227436P.
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                             backbone
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ABS77520/c
ID ABS77520 standard; DNA; 18
                                  RESULT 10
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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; ediabetuar glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting angiogenesis in a subject, involves administering at least antiangiogenic nucleic acid molecule to the subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Page 20; 276pp; English.
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                                                                                                                     1 AGAGGGUCGCACGCGGUA 18
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                                                                                    AGAGGGTCGCACGCGGTA 1
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                                                                                                                                                                                                                                                              invention
                                                                                                                                                         Conservative
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                                                                                                                                                                        88.9%;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis; diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telanglectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                ABL39077;
                                                                                                                                                                                                                                                                                                                               Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting angiogenesis in a subject, involves administering antiangiogenic nucleic acid molecule to the subject.
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                 Immunostimulatory nucleic acid SEQ ID NO:
                                                16-APR-2002
                                                                                                               ABL39077 standard;
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                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                 μ
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                 AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                  invention
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypertrophic scar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                               DNA; 18
                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                 Pred
                                                                                                                                                                                                                                                                                 Score 18; I
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                               6; Length 18,
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at least
                                                                                                                                                                                                                                                                  Gaps
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RESULT 12
AAL39192/c
ID AAL391
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                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                               breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin cancer, stomach cancer, testicular cancer, and uterine cancer. The present sequence is an immunostimulatory oligonucleotide described in
                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating or preventing cancer, such as basal cell carcinoma, comprises administering immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies to a subject having or at risk of
                                                             Murine Toll-like receptor related CpG DNA SEQ ID No 67
                                                                                                        AAL39192;
                                                                                                                                                                                                                                                                    Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                            treating or preventing cancer such as basal cell carcinoma, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer,
                                                                                                                                                                                                                                                                                                                                                                                                   of cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 218; 312pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody-induced cell lysis; cancer; immunostimulatory; CD20; angiogenesis; metastasis; cytostatic; phosphorothicate backbone; ss.
WO200222809-A2
                     Unidentified
                                         Murine Toll-like receptor; TLR9; TLR7; TLR8; ISNA; ds
                                                                                    05-SEP-2002
                                                                                                                            AAL39192 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                          exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-154611/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weiner G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2000; 2000US-0213346P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2001WO-US020154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                   Local
                                                                                                                                                                                 18
                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                          Similarity 88.9
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  surface antigens and antibodies. The methods are useful
                                                                                                                                                                                 AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                     AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hartmann G
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pom/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "phosphorothioate backbone"
                                                                                                                                                                                                                                    88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              base= OTHER
                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                             Score 18;
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                              DB 6; Length 18
                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                          o,
                                                                                                                                                                                                                                                                                                                                                                                         bladder
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                    the
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  EXEXEX SXEX GXE
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 13-NOV-1998;
                    06-AUG-2002.
                                         US6429199-B1
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RESULT 13
ABS70565/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and TIRB polypeptides. These polypeptides comprise fully defined
cequences of 1032, 1050 or 1032 amino acids as given in specification, or
their fragments, where TIRP, TIRP, and TIRB polypeptides or their
certagments have an amino acid sequence which is identical to human TIRP,
certagments have an amino acid sequence which is identical to human TIRP,
certagment cand of a murine TIR polypeptide. The isolated nucleic acids of the
acid of a murine TIR polypeptide. The isolated nucleic acids of the
certagment on are useful for inhibiting TIRP signalling activity in a cell.
certagment of TIRP polypeptides are useful for identifying nucleic acid
certagment. The polypeptides are also useful for identifying ISNA. The
certagment TIRP polypeptides are also useful for comparing TIRP,
certagment TIRP polypeptides are also useful for comparing TIRP,
certagment TIRP polypeptides are also useful for compounds) with
certagment TIRP, TIRB and TIRP polypeptides are also useful for
constantifying species specificity of an ISNA. The isolated nucleic acids of
continuous the titre to the invention are useful as probes or primers. This polypuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Synthetic
                                                        CpG; ss; dendritic cell; dendritic cell activation; cytostatic;
antiallergic; cancer; immunotherapy; infectious disease: allero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated murine Toll-like receptor (TLR)9, TLR7, TLR8 polypeptides, useful for identifying species specificity of immunostimulatory nucleic acid and identifying immunostimulatory nucleic acids.
                                                                                                                                                        Dendritic cell stimulating CpG oligodeoxynucleotide
                                                                                                                                                                                                                       25-NOV-2002
                                                                                                                                                                                                                                                                                      ABS70565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 76; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-393964/42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-2001;
22-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2001; 2001WO-US029229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002
                                                                                                                                                                                                                                                                                                                                              ABS70565 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents DNA relating to the isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (COLE-) COLEY PHARM GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to isolated murine Toll-like receptors (TLR)9, TLR7 TLR8 polypeptides. These polypeptides comprise fully defined tences of 1032, 1050 or 1032 amino acids as given in specification, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipford G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-0291726P
2001US-0300210P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0233035P.
2001US-0263657P.
                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wagner H;
                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toll-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors of
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98US-00191170.

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RESULT 14
ACD99318/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC This invention relates to a novel method for activating or causing CC maturation of a dendritic cell. The method comprises contacting a CC dendritic cell with an isolated nucleic acid containing at least one CC unmethylated CpG dinucleotide in an amount effective to activate or cause CC vivo. The method of the invention may have cytostatic or antiallergic CC activities. The method of the invention is useful for cancer CC immunotherapy or for treating an infectious disease or allergy, by CC administering an activated dendritic cell that express a specific cancer, CC microbial or allergy causing antigen, to a subject having a cancer concident of the allergy causing antigen or to a subject having an activated concident of the allergy causing antigen or to a subject having an activated concident of the allergy causing antigen or to a subject having an activated concident of the allergy causing antigen or to a subject having an activated concident of the allergy causing antigen or to a subject having an infection with a cc allergic reaction to the allergy causing antigen or to a subject having an infection with a cc allergic reaction to the allergy causing antigen of the invention. The method concident coll is prepared using the method of the invention. The method collective to activate the dendritic call is 8-80 bases in length in an amount effective to activate the dendritic call is 8-80 bases in length in an amount concident colls from the subject. The use of CpG allows the generation of concident colls from the subject of concident colls and isolating collective to activate the dendritic call is 8-80 bases in length in an amount collective to activate the dendritic call is 8-80 bases in length in an amount collective to activate the dendritic call is 8-80 bases in length in an amount collective to activate the dendritic calls to a subject, and isolating collective to activate to subject. The use of CpG allows the generation of concident and collective to activate to subject to subject to the allows the subjec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1994;
07-FEB-1995;
30-OCT-1996;
Synthetic
                                      Immunostimulatory; antiinflammatory; dermatological; antipsoriatic; antiulcer; gene therapy; vaccine; non-allergic inflammatory disease psoriasie; eczema; allergic contact dermatitis; latex dermatitis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss
                                                                                                                                                                                                                                                                                   ACD99318 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1997
                                                                                                                                                                                               25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Col 32; 52pp;
                                                                                                                                                 Immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infectious or allergy disease, by isolated nucleic acid containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA RES POUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a CpG oligonucleotide used in the method the invention
                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                    _
                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a dendritic cell for cancer immunotherapy or for treating or allergy disease, by contacting a dendritic cell with au ucleic acid containing at least one unmethylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hartmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-00276358.
95US-00386063.
96US-00738652.
97US-00960774.
                                                                                                                                                   nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%;
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                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
                                                                                                                                                   #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                 disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 15
ADB36390/c
ID ADB363
XX ADB363
XX ADB363
XX Immuno
XX Immuno
XX Immuno
XX Immuno
XX Os; al
KW hypo-x
XX Synthe
XX US2003
XX US2003
XX O2-FEE
XX O2-FEE
XX O2-FEE
XX (BRAT/
PA (PETE/
PA (POUR/
XX (FOUR/
XX (F
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a method of treating non-allergic inflammatc disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method useful for treating non-allergic inflammatory diseases, such as psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating non-allergic inflammatory diseases, such as psoriasis, allergic contact dermatitis, latex dermatitis or inflammatory b disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 8; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2002;
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                                                                             Bratzler RL,
                                                                                                                                                                                                                          03-FEB-2000; 2000US-0179991P.
                                                                                                                                                                                                                                                                           02-FEB-2001; 2001US-00776479.
                                                                                                                                                                                                                                                                                                                               08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                              US2003087848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunostimulatory nucleic acid #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypo-responsive
                                                                                                                                                      (BRAT/)
(PETE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BERG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KRIE/)
                                                                                                                               FOUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              allergy; asthma; poly-G nucleic acid; aerosol formulation;
o-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                          ) BRATZLER R :
) PETERSEN D I
) FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIEG A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berg DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                             Petersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                             Fouron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
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RESULT 16
ADB36433/c
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Matches 16
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                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma which comprises administering to a subject a poly in an aerosol formulation. The methods and compositions invention are useful for diagnosing and/or treating asthespecially in a hypo-responsive subject. The present sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                           Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represents
                                                                                                                                                                                          The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid
                                                                                                                                                                                                                                                Disclosure; Page 6; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                        (BRAT/)
(PETE/)
(FOUR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2001; 2001US-00776479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003087848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 5; 221pp; English.
                                                                                                                                                                                                                                                                                     Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                               WPI; 2003-657977/62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunostimulatory nucleic acid #47.
                                                                                                                   immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
   16;
                                                                                                                                                                                                                                                                                                                                                                                                                      ) BRATZLER R L.
) PETERSEN D M.
) FOURON Y.
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     Petersen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                   100.0%;
                                                                                                                   nucleic acid of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.98;
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                     Pred.
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                                       Score
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                     18;
                                                                                                                   the
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                                         BB
                                                                                                                   invention
                                     9;
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nucleic a
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allergy
 Gaps
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ADG68160/c
ID ADG681
XX ADG681
XX AC ADG681
XX DT 11-MAR
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AAD60215/c
ID AAD60215 standard; DNA;
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                                                                                            RESULT 18
                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                  The invention relates to a method of activating a dendritic cell. The method involves contacting the dendritic cell with an isolated nucleic acid containing at least one unmethylated CpG dinucleotide, where the nucleic acid is about 8-80 bases in length, in an amount that activates the dendritic cell. The compositions and methods of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                            Activating a dendritic cell useful for treating cancer, infectious diseases or allergies, comprises contacting the dendritic cell with an amount of an isolated nucleic acid that contains at least one unmethylated CpG dinucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide 1761
               11-MAR-2004
                                         ADG68160;
                                                                                                                                                                                                                                       Sequence 18 BP; 2
                                                                                                                                                                                                                                                                 useful for cancer immunotherapy, or for treating an infectious (e.g. viral, bacterial or fungal infections) or allergy. The inuseful in cell therapy. The present sequence is an oligonucleot for activating dendritic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-708674/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2002; 2002US-00161229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergy; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dendritic cell activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2003
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                                                                  ADG68160
                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 18; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1996;
30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FBB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IOWA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L5-JUL-1994;
                                                                                                                                                                                                                                                                ful in cell therapy. The activating dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
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                                                                                                                                                                                                 Similarity
                                                                  standard; DNA; 18
                                                                                                                                   AGAGGGTCGCACGCGGTA 1
                                                                                                                                                           AGAGGGUCGCACGCGGUA 18
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                                                                                                                                                                                      Conservative
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               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-00738652
97US-00960774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-00276358
95US-00386063
                                                                                                                                                                                                                                      A; 8 C; 4 G; 4 T; 0 U;
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                                                                                                                                                                                              88.9%;
                                                                                                                                                                                                              100.0%;
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                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer immunotherapy; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                              Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activating dendritic cells.
                                                                                                                                                                                                  No.
                                                                                                                                                                                                                BB
                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                               or allergy. The invent
is an oligonucleotide
                                                                                                                                                                                      0
                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                       Indels
                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                    activates
                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                                                                       Gaps
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Unmethylated

g G

dinucleotide-containing oligonucleotide

#58.

Unmethylated CpG dinucleotide; immune activation; Th1 pattern; cytokine production; NK lytic activity; B-cell proliferation; asthmatic disorder; autoimmune disorder; CpG-associated disorder; CpG-mediated leukocyte activation; endosomal acidification;

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                                                                  Query Match
Best Local S
Matches 16
                                                                                                                                                                    cc unmethylated CpG dinucleotide. The invention also relates to methods of control of the unit of the stimulating immune activation in a subject, where the stimulation is compensating a mucleic acid sequence of the invention, comprising control of the nucleic acid sequence acts as an adjuvant, a method of stimulating cytokine production in a subject comprising administering a nucleic acid sequence, a method of stimulating MK lytic activity in a converse of the invention, or optionally, where the nucleic acid sequence, a method of stimulating MK lytic activity in a subject comprising administering a nucleic acid sequence, a method of stimulating B-cell proliferation in a subject comprising administering a nucleic acid sequence, a method for treating a subject having an activity in a stimulating B-cell proliferation in a subject comprising administering an control of anticimulation of the control of a stimulating the control of a method for treating a subject having an activitical carrier, and a method for treating a subject having an autoimmune or other CpG-associated disorder by inhibiting CpG-mediated cardification in a pharmaceutical carrier. The methods are useful in correventing or treating autoimmune or other CpG-associated disorders, such as systemic lupus erythematosus, sepsis, inflammatory bowel disease, career or infections (e.g. viral, fungal, bacterial or parasitic infections). This sequence represents an oligonucleotide containing an unmethylated CpG dinucleotide, used in the scope of the invention.
                                                                                                                                           Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid sequence containing at least one unmethylated CpG dinucleotide, useful for preventing or treating autoimmune or other CpG-associated disorders, e.g. sepsis, arthritis, Grave's disease, asthm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       systemic lupus erythematosus; sepsis; inflammatory bowel disease; psoriasis; gingivitis; arthritis; Crohn's disease; Grave's disease; asthma; cancer; bacterial infection; viral infection; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 60; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-1997;
31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-1995;
30-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-2002; 2002US-00306522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-JUL-1994;
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18
                                                                    16;
                                                                                     Similarity
                            AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 95US-00386063.
; 96US-00738652.
; 97US-00960774.
; 2000US-00630319.
; 2002US-00187489.
                                                                                                                                         BP; 2
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n relates to nucleic acid sequences containing at least one CpG dinucleotide. The invention also relates to methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00276358
                                                                                                                                         A; 8 C; 4 G; 4 T; 0 U;
                                                                                  100.0%;
88.9%;
                                                                  2
                                                                                     Pred
                                                                                                     Score
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                     18;
                                                                                                                                         0 Other;
                                                                                                       멂
                                                                                                     10;
                                                                  0
                                                                                                     Length 18;
                                                                  Indels
                                                                  ç
                                                                  Gaps
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RESULT 19
ACF36780/c

ID ACF36780;

XX

ACF36780;

XX

ACF36780;

XX

ACF36780;

XX

DT 06-NOV-2003 (first entry)

XX

DE Immunostimulatory CpG oligonu

XX

Human TLR3; Toll-like receptor

XX

Human TLR3; Toll-like receptor

XX

Human TLR3; Toll-like receptor

XX

M02003031573-A2.

XX

PN W02003031573-A2.

XX

D1-APR-2003.

XX

COLE-2001; 2001US-0327520P.

XX

D3-OCT-2001; 2001US-0327520P.

XX

COLE-) COLEY PHARM GMBH.

XX

Lipford G;

XX

Lipford G;

XX

Disclosure; Page 18; 104pp; E

XX

Compound which comprises contoc

CC compound, the transduction

CC The invention relates to a me

CC compound which comprises contoc

CC sequence, or equals or exceed

CC sequence, or equals or exceed

CC sequence ACF36744-ACF36822 I

CC coligonucleotides which may be

CC according to the invention

XX

Sequence 18 BP; 2 A; 8 C; 4 G
ABIGULT 20
ADIO10/c
ID ADIO11
XX ADIO11
XX ADIO11
XX DIO11
XX DIO11
XX DIO12
AC ADIO16
XX CANCER
CX Immuno
XX Cancer
XW Antiba
XW Prosta
XW Prosta
XW bacter
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                                                                                                                                                                                                                                                                                                                                                                                                            문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening for species specificity of an immunostimulatory compound. Sequences ACF36744-ACF36822 represent exemplary immunostimulatory oligonucleotides which may be used to stimulate TLR3 signalling act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for identifying an immunostimulatory compound which comprises contacting a functional Toll-like receptor 3 (TIR3) with a test compound, and detecting a test response mediated by the TIR3 signal transduction pathway. A test compound is deemed to be immunostimulatory when the test response exceeds the negative control sequence, or equals or exceeds the reference response. The method is useful for identifying compounds that modulate TIR3 signalling activity, particularly immunostimulatory compounds. The method may also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying an immunostimulatory compound by contacting a functional Toll -like receptor (TLR) 3 with a test compound, and detecting a test response mediated by the TLR3 signal transduction pathway.
                                                                                                                                                                                                                                ADI01100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 18; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2001; 2001US-0327520P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TLR3; Toll-like receptor 3; TLR3 signal transduction pathway; immunostimulant; drug screening; CpG oligonucleotide; ss.
                                                                                                                                                                                                                                                                              ADI01100 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunostimulatory CpG oligonucleotide, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002WO-US031460.
                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; 8 C; 4 G; 4 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18; D
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
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cancer; immunostimulatory; cytostatic; virucide; fungicide; antibacterial; antiparasitic; antiasthmatic; brain; lung; ovary prostate; colon; leukaemia; carcinoma; sarcoma; tumour; viral; bacterial; parasitic; asthmatic; ss; CpG; unmethylated cytosine

ovary; breast;

Immunostimulatory

CpG-related oligodeoxynucleotide

. SEQ

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RESULT 21
ADM99069/C
ID ADM990
XX ADM990
XX ADM990
XX 29-JUL
XX Immuno
XX antial
KW antiin
KW dermat
KW dermat
KW unmeth
KW CpG ag
KW inflan
KW inflan
KW inflan
KW Thl in
XX Thl in
XX Thl in
XX Synthe
XX US2000
XX US2000
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Best Local S
Matches 16
                                                                                                                                         antiallergic; antiarthritic; antiasthmatic; antibacterial; antiinflammatory; antiparasitic; antipsoriatic; antithyroid; cytostati dermatological; fungicide; gastrointestinal; immunosuppressive; viruc; unmethylated CpG dinucleotide; asthmatic disorder; cancer; infection; allergy; endosomal acidification; autoimmune disorder; cpc associated disorder; systemic lupus crythematosus; sepsis; CpG associated disorder; systemic lupus crythematosus; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiparasitic and antisthmatic activities and may be useful for treating or preventing cancer, including brain, lung, ovary, breast, prostate and colon cancers, as well as leukaemia, carcinoma, sarcoma and tumour. Furthermore, the method may be utilised to address viral, fungal, bacterial or parasitic infection and asthmatic disorders. The current sequence is that of the immunostimulatory CpG (unmethylated cytosine-guanine)-related oligodeoxynucleotide (ODN) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Immunostimulatory CpG containing oligonucleotide segid 60
                                                                                                                                                                                                                                                                                                                                 ADM99069
                                                                                                                                                                                                                                                                                                                                                                ADM99069 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention has cytostatic, virucide, fungicide, antibacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method whereby cancer is treated prevented by administering an immunostimulatory nucleic acid. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treatment and/or prevention of cancer and other disorders, e.g. tumor and viral infection, involves administering an immunostimulatory nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-2003.
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                                  US2004087538-A1
                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krieg AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-1995;
30-OCT-1996;
                                                                                                                  Crohn's disease; Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IOWA ) UNIV IOWA RES FOUND
                                                                                                                Inflammatory bowel disease; psoriasis; gingivitis; arthritis;
Crohn's disease; Grave's disease; asthma; lymphocyte activati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L5-JUL-1994;
                                                                                                 immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiher G;
                                                                                                 response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00276358.
95US-00386063.
96US-00738652.
97US-00960774.
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                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
                                                                                               response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12;
                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                               cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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method
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06-MAY-2004

Synthetic

US2004106568-A1

25-JUL-2003; 2003US-00627331.

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ADO0478/c
ID ADO047
XX ADO047
XX ADO047
XX ADO047
XX ADO047
XX Unmeth
XX Astem
XX Aste
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Best Local S
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30-OCT-1996;
30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes an isolated nucleic acid sequence containing at least one unmethylated CpG dinuclectide. The nucleic acid is useful for treating an asthmatic disorder, and may also be used for treating cancer, viral, fungal, bacterial, or parasitic infections. The nucleic acid may also be used for treating allergies, and as a synthetic adjuvant. Administration of an inhibitor of endosomal acidification is useful for treating autoimmune or other CpG associated disorders, such as systemic lupus crythematosus, sepsis, inflammatory bowel disease, psoriasis, giggingivitis, arthritis, Crohn's disease, Grave's disease and asthma. This
                                                                                                                                                                                                                                                                                                                                                                     natural killer cell lytic activity; NK; B cell proliferation; asthmatic disorder; autoimmune disorder; CpG associated disorder; systemic lupus crythematosus; sepsis; inflammatory bowel disease;
                                                                                                                                                                                                                                                                dermatological; immunosuppressive; antiarthritic; antithyroid; cytost
                                                                                                                                                                                                                                                                                                                    psoriasis; gingivitis; arthritis; Crohn's disease; Grave's di
cancer; viral; fungal; bacterial; parasitic; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unmethylated CpG dinucleotide; immune response; T helper cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CpG oligonucleotide #60 tested for immunostimulatory activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD004787;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 60; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid sequence containing at least one unmethylated CpG dinucleotide, useful for treating autoimmune or other CpG associated disorder, e.g. systemic lupus erythematosus, sepsis, psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-374746/35.
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                                                                                                                                                                                                                                     antiparasitic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IOWA ) UNIV IOWA RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents an immunostimulatory CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mmune activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₩,
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96US-00738652.
97US-00960774.
99US-00337619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokine production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; I
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                            antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                         Grave's disease;
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RESULT 23
ADU89320/c
ID ADU893
XX ADU893
XX ADU893
XX ALlerg
XX Allerg
XX Allerg
XX Allerg
XX Antiba
KW antiba
KW immunc
KW bacter
XX Synthe
XX US2004
XX US2004
XX PP US2004
XX PP 23-APF
XX PP 03-PEE
PR 03-PEE
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1997;
31-JUL-2000;
02-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to oligonucleotide sequences containing at least one unmethylated CpG dinucleotide that are able of modulating an immune response such as stimulating Thelper cell (Th) pattern of immune activation, cytokine production, natural killer cell (NK) lytic activity, and B cell proliferation in subject, preferably human. The immunostimulatory oligonucleotides of the invention are useful for treating asthmatic disorders, autoimmune or other CpG associated disorders (e.g. systemic lupus erythematosus, sepsis, inflammatory bowel disease, psoriasis, gingivitis, arthritis, Crohn's disease, Grave's disease, cancer, and viral, fungal, bacterial, and parasitic diseases. The present sequence represents an unmethylated CpG dinucleotide colligonucleotide that is tested for its ability to modulate an immune
   03-FEB-2000;
02-FEB-2001;
                                                                                                                                                                                                                                                                                                                            ADU89320 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequence containing unmethylated cytosine-guanine dinucleotide, useful for modulating immune response, e.g. stimulati pattern of immune activation, cytokine production, or B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSU)
                                            23-APR-2004; 2004US-00831778
                                                                                                      US2004235774-A1
                                                                                                                                                                                        ss; antiasthmatic; antiallergic; dermatological; antiinflammatory;
antibacterial; virucide; immunoglobulin B antagonist; allergy;
                                                                                                                                                                                                                                                                                                  ADU89320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-419485/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krieg
                                                                         25-NOV-2004
                                                                                                                                                                                                                                      Allergic response
                                                                                                                                                                                                                                                                   10-FEB-2005
                                                                                                                                                                            immunostimulator; asthma; rhinitis; urticaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                                                                                                                                                      18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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US DEPT HEALTH & HUMAN
COLEY PHARM GROUP INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                      AGAGGGTCGCACGCGGTA 1
                                                                                                                                                              infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IV IOWA RES FOUND.
DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 94US-00276358.
; 95US-00386063.
; 96US-00738652.
; 97US-00960774.
; 2000US-00630319.
; 2002US-00187489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 2000US-0179991P
2001US-00776479
                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                      suppressor oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steinberg
                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72pp; English.
                                                                                                                                                                                                                                                                                                                            ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>۰</u>
                                                                                                                                                                             dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g. stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 24
ADU89372/c
PACE X PACE X PROPERTY PACE X 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and stopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss; antiasthmatic; antiallergic; dermatological; antiinflammat antibacterial; virucide; immunoglobulin B antagonist; allergy; immunostimulator; asthma; rithinitis; urticaria; dermatitis; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suppressing allergies, dermatitis, in a subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Allergic response suppressor oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADU89372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4; 235pp; English.
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                                               WPI; 2004-833006/82.
                                                                                                                                                                                                                                                    03-FEB-2000; 2000US-0179991P
02-FEB-2001; 2001US-00776479
                                                                                                                                                                                                                                                                                                                               23-APR-2004; 2004US-00831778.
                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004235774-A1
                                                                                                                                                                          (BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRAT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  essing allergies, including asthma, rhinitis, urticaria atitis, in a subject, comprises administering a first and immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                               ) BRATZLER R
) PETERSEN D |
FOURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PETERSEN
FOURON Y.
                                                                                               RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGGGTCGCACGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petersen
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                                                                                               Petergen
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18; I
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhinitis, urticaria and atopic
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Suppressing allergies,

including asthma, rhinitis, urticaria and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleic acid-bearing composite; liposome; 2-0-(2-diethylaminoethyl)carbamoyl-1,3-0-dioleoylglycerol; pharmaceutical; oncogene; bol-2; cancer; viral infection; cytostatic; virucide; antiinflammatory; gene therapy; phos
                                                                                                                                                                                                                                                                                                                                            Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 de to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral
Oligonucleic acid-bearing composite, useful for treating cancer, comprises cationic liposome composed of 2-0-(2-diethylaminoethyl)carbamcyl-1,3-0-diolecylglycerol and phospholi active ingredient with oligonucleic acid.
                                                                                                                                                          30-MAY-2003; 2003JP-00154798.
12-NOV-2003; 2003JP-00382819.
31-MAR-2004; 2004JP-00104036.
                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatitis, in a subject, comprises administering a first and second dose of an immunostimulatory nucleic acid
                                                                                                                                                                                                                   28-MAY-2004; 2004WO-JP007785
                                                                                                                                                                                                                                                                            WO2004105774-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reverse sequence of Bcl-2 antisense DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADV11411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADV11411 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 medicaments. They can also be used in preventing bacterial and vira infections. This sequence represents an oligonucleotide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                (NNSH ) NIPPON SHINYAKU CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response in a subject by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 88.9
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                                                                                                   Hirabayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 56; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to a
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                       base=
                                                                                                                                                                                                                                                                                                      "OTHER=Phosphorothioate backbone"
                                                                                                  Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method of suppressing
                                                                                                                                                                                                                                                                                                                       OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
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                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uppressing a symptom of an allergic a first and second dose of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                   il infection; inflammation;
therapy; phosphorothicate;
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             and phospholipid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interfering RNA), shrNA, antisense DNA, antisense RNA, DNA enzyme, cribozyme or an aptamer. The oligo double-stranded RNA comprises an entisense and sense RNA strand with 2 DNA bases at the 3' terminal ends. The oligonucleic acid-bearing composite is delivered into a cell containing a target molecule (e.g. target DNA, RNA or protein). The containing a target molecule (e.g. target DNA, RNA or protein). The containing a target molecule (e.g. target DNA, RNA or protein). The containing a target molecule (e.g. target DNA, RNA or protein). The containing a target molecule (e.g. target DNA, RNA or protein). The containing a target molecule of the oligonuclectide includes a viral gene of HIV, composition for transition related gene such as Dcl-2, composite (tumor necrosis factor alpha) and Fas gene, their transcription product, compositation product, and the non-coding region of genomic DNA of arbitrary protein. The oligonucleic acid-bearing composite is useful for preparing a pharmaceutical composition for treating or preventing diseases such as concern, viral disease or inflammatory disease. The oligonucleic acid enables efficient biological activity with respect to the target molecule (e.g. target DNA, RNA or protein). This sequence represents the reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    target DNA, target RNA or target protein. The oligonucleic acid-bearing composite has an average particle diameter of 10-100 nm. In the preferred oligonucleic acid-bearing composite the phospholipid is lecithin, the oligonucleotide is RNA, DNA or its derivative, preferably siRNA (short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disclosed is a pharmaceutical composition for preventing and/or treating disease, comprising the oligonucleic acid-bearing composite, where the target molecule for the oligonucleic acid-bearing composite, includes the composite of the oligonucleic acid-bearing composite, includes the composite of the oligonucleic acid-bearing composite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleic acid-bearing composite comprising a cationic liposome composed of 2-O-(2-diethylaminoethyl)carbamoyl-1,3-O-dioleoylglycerol and phospholipid as an active incredient, with the oligonucleic acid having 10-15 bases. Also
11-MAY-1993;
                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                      miac
                                                                                                                                                                                                                                                                                                                Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial immunomodulatory CpG oligoribonucleotide, SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADW79934 standard; RNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 6;
                                  15-MAR-2004; 2004US-00800926
                                                                                                               US2005032731-A1
                                                                                                                                                                                                                                                                                                                                                                       endotoxic shock; antibacterial; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                      Immune modulation; immune stimulation; bacterial infection; infection;
                                                                            10-FEB-2005.
                                                                                                                                                                                                                                                                                                                                                     immunostimulant; adjuvant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                      feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
93US-00059745
                                                                                                                                                                                             /note= "
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                         . "CpG
                                                                                                                                                      "CpG dinucleotide
                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                 dinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멂
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                         immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 27
ADZ88546/c
ID 89546/c
ID ADZ885
XX
AC ADZ885
XY
DT 14-JUL
XX
DE CPG OD
XX
Immune
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                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc adapted a non-toxic planting response to their release from bacteria. The circular planting response to their release from bacteria. The circular planting response to their release from bacteria. The convertion also relates to ame thod for the preparation of the bacterial convertion and planting the separating critical convertions of the separating critical convertions and media from the bacteria, and filtering the separated product to remove substances with a molecular weight of more that 10 kD; and a critical criti
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JAN-1995;
18-AUG-1995;
29-OCT-1996;
17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a composition for modulating and/or stimulating the immune system of an animal, comprising bacterial oligoribonucleotides (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are preferably ADW79934-ADW79936, contain CpG motifs and are resistant to RNase. Bacteria produce RNAse-resistant CpG ORNs in response to stresses such as a change in environment, including the neutral pH they encounter when they colonize animals. The immune systems of animals have co-evolved when they colonize animals. The immune systems of animals have co-evolved to recognize such CpG ORNs as being derived from bacteria, and has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition for modulating and/or stimulating immune system of animal useful for withstanding microbial infections and lethality of endotoxic shock, comprises low molecular weight oligoribonucleotide from bacteria.
                                                 CpG ODN1761,
                                                                                                                                                       ADZ88546;
                                                                                                                                                                                                      ADZ88546 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing them are non-toxic. The present sequence represents specifically claimed bacterial CpG oligoribonucleotide present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marshall
Immune stimulation; immunotherapy; nucleic acid vaccine,
                                                                                                   14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-161694/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; SEQ ID
                                                                                                                                                                                                                                                                                                                                   _
                                                                                                                                                                                                                                                                                                                                                                          1 AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                              AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 95US-00376175.
; 95US-00517016.
; 96US-00739264.
; 98US-00193653.
; 2001US-00883550.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                              to induce NK cell lytic activity, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO 1; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 4 C; 8 G; 0 T;
                                                                                                                                                                                                      DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 18; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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AEA16652/c
ID AEA166
XX
AC AEA166
XX
DT 14-JUL

AEA16652 standard; DNA; 18 BP

AEA16652;

14-JUL-2005

(first entry)

밁 S

18 ш

AGAGGGUCGCACGCGGUA 18 AGAGGGTCGCACGCGGTA

Query Match Best Local S Matches 16

Local Similarity

100.0%;

Conservative

2

Pred. No. 10; 2; Mismatches Score 18;

0

Indels

<u>,,</u>

Gaps

0

DB 14; Length 18;

Sequence 18

BP; 2

?

8 C; 4 G; 4 T; 0 U; 0

Other;

RESULT 28

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response from antibody (humoral) immune response (Th2) to cellular immune response (Th1) thus acting as immune subject compounds. The invention is useful for treating, preventing or ameliorating a papilloma virus infection, autoimmune disorders (particularly systemic lupus) and other disorders such as tumor or cancer, viral, crythematosus) and other disorders such as tumor or cancer, viral, crythematosus) and other disorders such as tumor or cancer, viral, creation and leukemia and for stimulating immune activation. The nucleic acid sequences of the invention are useful as an adjuvant for generating antibodies and in the production of vaccines. The invention is also useful in immunotherapy. The present sequence is a CpG oligonucleotide involved in induction of natural killer (NK) cell lytic activity. Note: The present sequence is the SEQ ID NO: 60 which is given in the sequence listing. This sequence differs from the SEQ ID NO: 60 shown in the cdisclosure (page 19) of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating, preventing or ameliorating a papilloma virus infection comprises administering to the subject a composition containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal infection; fungicide; parasitic infection; antiparasitic;
bacterial infection; antibacterial; asthma; antiasthmatic; inflammation;
respiratory disease; leukemia; hematological disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  papillomavirus infection; virucide; infection;
systemic lupus erythematosus; antiinflammatory; dermatologis
immunosuppressive; dermatological disease; immune disorder;
metabolic disorder; musculoskeletal disease; tumor; cytosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 60; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1994;
07-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005101554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unmethylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1996;
30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klinman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 96US-00738652.
; 97US-00960774.
; 2000US-00630319.
; 2002US-00187489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CpG dinucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003US-00627413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to unmethylated cytosine-guanine (CpG) that activate lymphocytes and redirect a subject's immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00276358.
95US-00386063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinberg AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dermatological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; neoplasm;
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Unidentified.

antibacterial;

fungal

allergic rhinitis; inflammation; urticaria; autoimmune disease; immunosuppressive; systemic lupus erythematosus; metabolic disomusculloskeletal disease; tumor; cancer; cytostatic; neoplasm; hematological disease; viral infection; bacterial infection;

cytostatic; neoplasm; leukemia;

parasitic infection;

asthma; antiasthmatic; phosphorothicate;

infection; fungicide;

ear, nose,

antiallergic; eczema; dermatological; antiinflammatory; dermatological disease; immune disorder; common cold; v

throat disease; infection; respiratory disease

virucide;

Immune stimulation; immunotherapy; nucleic acid vaccine; allergy;

S-ODN 1761 SEQ

ID NO:

CpG immunostimulatory oligo,

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                    5
                                                         Query Match
Best Local (
                                               Matches
                                                                                                                                                     The present invention relates to nucleic acid sequences containing at least one unmethylated CpG dinucleotide which are immunostimulatory. The invention also provides a method for desensitizing a subject against the occurrence of an allergic reaction in response to contact with an allergen. The method involves administering to a subject an amount for desensitizing the subject against the occurrence of an allergic reaction of an immunostimulatory nucleic acid. The invention is useful for treating or preventing allergy and allergic conditions selected from eczema, allergic rhinitis, allergic coryza, hay fever, urricaria and food allergy. The invention is also useful for treating autoimmune disorder particularly systemic lupus erythematosus and other disorders, e.g. tumor or cancer, viral, bacterial, fungal, or parastic infection, asthmatic
                                                                                                        disorder, or leukemia in a subject and for producing vaccine. sequence is a CpG immunostimulatory phosphorothicate modified oligodeoxynucleotide (S-ODN).
                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 60; 72pp; English
                                                                                                                                                                                                                                                                                                                                              nucleic acid.
                                                                                                                                                                                                                                                                                                                                                       Desensitizing a subject comprises administering
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-345417/35
                                                                                                                                                                                                                                                                                                                                                                                                                    Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                    AM.
18
                                                            Similarity
                                                                                              18
                     AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                    Kline JN;
                                                                                             BP;
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004US-00921086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-00276358.
95US-00386063.
96US-00738652.
97US-00960774.
99US-00337584.
                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                             ۶,
                                                                                              8 C; 4 G;
                                                          88.9%;
                                                                      100.
                                                                                                                                                                                                                                                                                                                                                       against the occurrence to a subject an amount
                                             2
                                                            Pred.
                                                                    Score
                                                                                             4
                                             Mismatches
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                                                                    18;
                                                                                              0
U;
                                                                                              0 Other;
                                                                      DB 14; Length 18;
                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                        an of
                                               Indels
                                                                                                                                                                                                                                                                                                                                                        an allergic reaction immunostimulatory
                                             0;
                                                                                                                                           The present
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Bcl-2/CRB 21-OCT-2002 ABK90354;

hybrid antisense oligonucleotide

BK1-PS+1084.

(first entry)

Antisense; ss; probe; Bcl-2; cell proliferative disorder; cAMP response element; bacterial infection; viral infection

infection;

cancer; CRE;

anaphylaxis; allergy; arthritis; sorder; parasitic infection; virue

cAMP response inflammation;

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RESULT 30
ABK90354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 29
                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                 modulates an immune response including a Th1 pattern of immune activation, cytokine production, natural killer (NK) lytic activity and cell proliferation. The oligonucleotide is useful for stimulating an immune response including a Th1 pattern of immune activation, cytokine production, NK lytic activity and B cell proliferation, in a subject having cancer or an infectious disease. The invention is also useful as synthetic adjuvant and in immunotherapy. The present sequence is a CpG oligonucleotide involved in the induction of NK lytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New oligonucleotide, useful for stimulating an immune response a Th1 pattern of immune activation, cytokine production, NK lytactivity and B cell proliferation, in a subject having cancer cativity and B cell proliferation, in a subject having cancer cativity.
                                                                                                                                ABK90354
                                                                                                                                                                                                                                                                                           Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-590434/60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krieg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAR-2005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2005182017-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic; neoplasm; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NK lytic activity inducing CpG oligo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEC16249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEC16249 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an immunostimulatory oligonucleotide that
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 60; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1999;
14-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immune stimulation; cell proliferation; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IOWA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infectious
                                                                                                                                                                                              18
                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                         Similarity
                                                                                                                               standard; DNA; 57
                                                                                                                                                                                            AGAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease.
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00960774.
99US-00337893.
2003US-00619279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2005US-00071836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                         88.98;
                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                     Score 1.
                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antimicrobial;
                                                                                                                                                                                                                                                     a 18;
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ODN 1761,
                                                                                                                                                                                                                                                                    DB 14; Length 18;
                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorothicate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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RESULT 31
AAQ86651/c
ID AAQ866
XX AAQ866
XX DT 25-MAR
DT 27-SEP
XX DE BC1-2
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl response element (CRE) sequence and a sequence that hybridises to the bcl pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of cancer cells in vitro, which comprises contacting the cancer cells with a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; (2) treating or preventing cancer in a human, which comprises administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral
                                                 25-MAR-2003
27-SEP-1995
                                                                                                  AAQ86651;
                                                                                                                                AAQ86651 standard;
                                                                                                                                                                                                                                                                                                                                                                                          bcl-2 antisense oligomer are also useful for preventing or treating hepatitis B virus infection. The hybrid oligomers can also be used for screening candidate transcription factors or other molecules e.g., gene regulatory proteins or for diagnostic assays. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid oligomer comprises a cyclic AMP response element sequence and sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
               Bcl-2 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                          Sequence 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klem RE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2001; 2001US-0263244P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JAN-2002; 2002WO-US001967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200257480-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified_base
                                                                                                                                                                                                                                                                                                                                                                           3cl-2/CRE hybrid antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENT-) GENTA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-590754/63
                                                                                                                                                                                                                  37
                                                                                                                                                                                                                                               _
                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                             AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                AGAGGGTCGCACGCGGTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 58; 78pp; English
                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                               Conservative
                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                            12 A; 17 C; 18 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatitis B infection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                DNA; 17
                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                BP
                                                                                                                                                                                                                                                                             N
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                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                          Score 18;
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                            10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          DB 6; Length 57;
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                             0
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RESULT 32
ABK90272/c
ID ABK902
XX ABK902
XX ABK902
XX ABC1-2-
XX ANTise
KW ANTise
KW CAMP r
KW Inflam
KW autoim
KW autoim
KW tumour
XX Homo s
YN W02002
XX W2-JAN
XX 22-JAN
XX 22-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          닭
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense oligonucleotides were tested for their ability to induce programmed cell death (DNA fragmentation) in the human lymphoma cell line RS11846. The oligonucleotides are phosphodiesters targeted against the translation initiation site (AAQ86650-55) or the 5'-cap region (AAQ86656-58) of human bcl-2 pre-mRNAs. The AAQ86651 oligonucleotide provided pronounced DNA fragmentation. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                    autoimmune disorder; parasitic tumourigenesis; hepatitis B inf
                                                                                                                                                            Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cycostatic;
                                                                                                                                                                                                                 Bcl-2-targeting antisense oligonucleotide #9.
                                                                                                                                                                                                                                                                      ABK90272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 12; Page 33; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-139394/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy; lymphoma; programmed cell death; ss.
                           22-JAN-2002; 2002WO-US001967.
                                                                                WO200257480-A2
                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                ABK90272 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9508350-A1
                                                       25-JUL-2002
                                                                                                                                                                                                                                             21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REED/) REED
                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                  GAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                         GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ი
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00124256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US010725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mote= "3'-5' (antisense) sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                94.4%;
                                                                                                                                                                                                                                                                                                 뫄
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17;
Pred. No.
                                                                                                                                    infection; virucide; hyperplasia;
mection; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 17
                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                         cancer, CRE;
                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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22-JAN-2001; 2001US-0263244P.

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
           05-JUN-1995;
18-MAY-1998;
17-AUG-1999;
                                                         22-DEC-1988;
21-FEB-1992;
20-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer cells in vitro, which comprises contacting the cancer cells with a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; (2) treating or preventing cancer in a human, which comprises administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer and a bcl-2 antisense oligomer and a CRE decoy oligomer and a carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer,
                                                                                                                                                                                                                                             Antisense oligonucleotide; B cell cancer; lymphoma; leukemia; chemot autoimmune disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bcl-2 antisense oligomer are also useful for preventing or treating because in the virus infection. The hybrid oligomers can also be used for screening candidate transcription factors or other molecules e.g., gene regulatory proteins or for diagnostic assays. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid oligomer comprises a cyclic AMP response element sequence and a sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl
                                                                                                                     28-NOV-2000;
                                                                                                                                                      02-JUL-2002
                                                                                                                                                                                    US6414134-B1
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                           Antisense oligodeoxynucleotide of the human bcl-2 gene
                                                                                                                                                                                                                                                                                                                                            25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                        ABQ78530 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -2 pre-mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENT-) GENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or mRNA. Also included are:
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                       2000US-00724426
                        88US-00288692.
92US-00840716.
93US-00124256.
95US-00465485.
98US-00080285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 A; 8 C; 4 G; 3 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.48;
88.28;
                                                                                                                                                                                                                                                               chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                            lymphoma/leukemia-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1) inhibiting the growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                              gene; bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                             purging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of.
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RESULT 34
ABL54157/c
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                       25-AUG-2000;
29-SEP-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is useful for inhibiting cancer cell (lymphoma or leukemia cells) growth, for increasing the sensitivity of cancer cells to cancer chemotherapeutic agents, or for inducing cancer cell death alone or in combination with any one or more cancer chemotherapeutic agents. It is also useful for reducing the bcl-2 gene expression or impairing bcl-2 protein function, for ex vivo bone marrow purging, for removing residual malignant cells from the bone marrow, for inhibiting cancer of neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia -2 mRNA, useful for inhibiting cancer cell growth, for treating autoimmune disorders, and for ex vivo bone marrow purging.
                                                                                       Warrel RP,
                                                                                                                                                                                                                       07-MAR-2002.
                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                    B cell lymphoma/leukaemia-2; bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                            Bcl-2 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL54157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL54157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Col 17; 41pp; English
                                                                                                                                                                                          23-AUG-2001; 2001WO-US026414
                                                                                                                                                                                                                                               WO200217852-A2
                                                                                                                                                                                                                                                                                                                            breast cancer; ovarian cancer; prostate cancer; renal ce
hepatoma; bile duct carcinoma; choriocarcinoma; cervical
                                                                                                                                                                                                                                                                                                                 testicular
                                                                                                                                                                                                                                                                                                                           hepatoma; bile duct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYPE-) UNIV PENNSYLVANIA
                                                                                                                 (GENT-) GENTA INC.
                                                                                                                                                                                                                                                                                                                                                      eukaemia; colon carcinoma; rectal carcinoma; pancreatic
                                                                                                                                                                                                                                                                                                  and neck cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         growth,
                                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGGTCGCACGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGGUCGCACGCGGUA 18
                                                                                       Klem RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                         2000US-0227970P.
2000US-0237009P.
2000US-00709170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for treating autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 8 C; 4
                                                                                                                                                                                                                                                                                                   lung carcinoma; bladder carcinoma;
er; brain cancer; cytostatic; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents an antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17; DB Pred. No. 35; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  oncogene; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                        cell carcinoma;
                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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<u>,</u>

high doses for

or preventing cancer, tumors and carcinomas, comprises ering B cell lymphoma/leukemia-2 antisense oligonucleotide es for short period for time with one or more cancer

at

Treating

Disclosure; Page 54; 64pp; English.

The present sequence is that of a B cell lymphoma/leukaemia-2 (bcl-2)

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RESULT 35
ADT93917/c
ID ADT939
XX ADT939
XX ADT939
XX ADT939
XX Se; Cy
KW Se; Cy
KW multip
KW tumor
KW antise
XX Synthe
XX WO2004
XX O9-APR
XX O9-APR
XX (ENZO-
XX WPI; 2
XX WPI; 2
XX New pc
PT reager
XX New pc
PT New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in significant therapeutic responses, including low toxicity, high to tolerance and prolonged survival. Administration at high doses for short periods of time (less than 14 days) also provides significant therapeutic responses in the treatment of cancer. The bol-2 antisense oligomer may also be used to increase the sensitivity of a subject to cancer therapeutics, and in combination with hormone treatment or gene therapy. Conditions that may be treated or prevented include cancer of the chematopoietic system, skin, bone and soft tissue, reproductive system, genitourinary system, breast, endocrine system, brain, central nervous system, peripheral nervous system, kidney, lung, respiratory system, contractive system, peripheral nervous system, kidney, lung, respiratory system, contractive system, peripheral nervous system, kidney, lung, respiratory system, contractive system, peripheral nervous system, kidney, lung, respiratory system, contractive system, peripheral nervous system, kidney, lung, respiratory system, contractive system, peripheral nervous system, kidney, lung, respiratory system, contractive system, kidney, lung, respiratory system, contractive system, contractive system, kidney, lung, respiratory system, contractive system, contractive system, kidney, lung, respiratory system, contractive syst
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-APR-2003; 2003US-0462070P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-2004; 2004WO-US010852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; cytostatic; hepatotropic; virucide; anti-HIV; cancer; multiple myeloma; chronic lymphocytic leukemia; metastasis; neoplasm; tumor growth; neoplastic growth; liver disease; viral disease; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense oligonucleotide. The present invention is directed to the use of bcl-2 antisense oligomers, particularly G3139 (see ABL54148), to treat and prevent bcl-2 related disorders. Administration at high doses results
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004092191-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT93917 standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanoma (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ENZO-)
                                                                                                                                                                                                                                                                                                                                                                                                   ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                   Greenwald RB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligonucleotide #5 for oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               choriocarcinoma, lung carcinoma, bladder carcinoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Pred. No. 35;
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Mismatches

<u>.</u>

0,

Gaps

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The invention relates to novel polymeric oligonucleotide prodrugs

of f

Example 12; SEQ ID NO 9; 41pp; English

Treating

g cancer, e.g. non-Hodgkin's lymphoma, prostate cancer, or breast by administering an amount of anticode oligomer for treating the

Disclosure; SEQ ID NO 5; 89pp; English

New polymeric oligonucleotide prodrugs useful as diagnostic and analytic reagents, and as therapeutic agent for the treatment of cancer.

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RESULT 36
ADW13838/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC formula: R2-(L4)p-(L3)m-X1-(L2)n-(L1)o-R1 (I) and (X1-L2)u'-T1 (II) where CC R1 and R2 = H or polymer residue; L1 and L4 = relesable linking moieties; CC L2 and L3 = spacing group; X1 = nuclectide or oligonuclectide residue; T1 CC = R61-CH2-C(0)-NH-CH(C(0-D')-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', R61-CH2-C(0)-D', CH2-C(0)-D', 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 15
                                                                                                                                                                              Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastrointestinal tumor; colon tumor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; bcl-2; chemotherapy; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-2 antisense oligodeoxynucleotide, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADW13838;
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                                                                                                                                     WPI; 2005-072307/08
                                                                                                                                                                                                                                                                                                                                           21-FEB-1992;
20-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6841541-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADW13838 standard; DNA; 17
                                                                                                                                                                                                                                                            22-DEC-1998;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                   05-JUN-1995;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-hodgkin lymphoma; prostate tumor; breast tumor;
                                                                                                                                                                                                                    (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGTCGCACGCGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGGUCGCACGCGGUA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                         2000US-00724425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                   92US-00840716.
93US-00124256.
95US-00465485.
98US-00080285.
                                                                                                                                                                                                                                                            98US-00288692.
99US-00375514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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RESULT 37
AAH48722/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                         New conjugates of oligonucleotides with somatostatin analogs, antisense therapy, e.g. of viral, inflammatory or asthmatic d especially tumors overexpressing the somatostatin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical carrier; and increasing the sensitivity of a tumor cell to a chemotherapeutic agent. The anticode oligomers have cytostatic activity. The oligomers may be used in gene therapy to treat cancer. The method is also useful for increasing the sensitivity of a tumor cell to a chemotherapeutic agent. The types of treatable cancer include non-lodgkin's lymphoma, prostate cancer, breast cancer, gastro-intestinal cancer, or colon cancer. The anticode oligomers are useful for inhibiting growth of cancer cells or killing tumor cells. This polynucleotide sequence represents a bcl-2 oligodeoxynucleotide of the invention.
                                                                                                                                                                              Eisenhut M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer; phosphorothioate; somatostatin; cytostatic; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH48722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH48722 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expressin pharmaceutical
    Example 3;
                                                                                                                                  WPI; 2001-530596/59.
                                                                                                                                                                                                                                                                   14-FEB-2000;
                                                                                                                                                                                                                                                                                                               14-FEB-2000; 2000DE-01006572
                                                                                                                                                                                                                                                                                                                                                                                                      DE10006572-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proto-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
                                                                                                                                                                                                                          (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rising the administration of anticode oligomers for treating k expressing cancer cells. The invention further comprises: a maceutical composition comprising an anticode oligomer, and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGUCGCACGCGGUA 18
Page 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                            Mier W,
                                                                                                                                                                                                                                                                     2000DE-01006572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ry; antiasthmatic; cardiant; antisense therapy; inflammatory process; somatostatin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system disease; cardiovascular disease; bcl-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
/mod_ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
16pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated primer SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    base= OTHER
                                                                                                                                                                            Britia R,
                                                                                                                                                                                                                                                                                                                                                                                                                                             "phosphorothioate"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17;
                                                                                                                                                                              Haberkorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method for treating cancer in a human, anticode oligomers for treating bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멂
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                                                                  disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                  useful in isease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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complementary to

of an

at least part of the sequence

acid sequence; of which

and (b)

18 comprising

novel oligonucleotide conjugate (I)

This invention describes a

an oligonucleotide,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ86650/c
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung tumors, breast tumors, brain tumors or other endocrine tumors), but are also useful for treating viral diseases (e.g. herpes simplex-1 infection), inflammatory disease (typical target RNA the NA the NF-kappa-B), asthmatic disease (typical target RNA the adenosine Al receptor), centra nervous system disease (typical target RNA c-myc). (I) are efficiently taken up by cells and incorporated in target cells (via the SSTR) and are highly selective for cells overexpressing SSTR's. This sequence represents a primer used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of (I) is
disease, i
                                                                                                                                                                             Reed
                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of (I) is claimed in antisense therapy, especially of cancer, v disease, inflammatory processes or asthmatic, central nervous s cardiovascular disease. (I) are especially used for therapy of
          58) of human field.)
                                                       Antisense oligonucleotides were tested for their abilit programmed cell death (DNA fragmentation) in the human
                                                                                                                                                      WPI; 1995-139394/18
                                                                                                                                                                                                                           20-SEP-1993;
                                                                                                                                                                                                                                                  20-SEP-1994;
                                                                                                                                                                                                                                                                         30-MAR-1995.
                                                                                                                                                                                                                                                                                                  WO9508350-A1
                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                          Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; lymphoma; programmed cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl-2 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
27-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ86650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ86650 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       virucide, antiinflammatory, antiasthmatic and cardiant activity. The use
                               RS11846. The oligonucleotides are phosphodiesters translation initiation site (AAQ86650-55) or the 5
                                           programmed
RS11846. Th
                                                                                          Example 12; Page 33; 108pp; English
                                                                                                                   solid
                                                                                                                           Anti-code oligomers
                                                                                                                                                                                                   (REED/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                 tumours,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                 евр.
                                                                                                                                                                                                                            93US-00124256.
                                                                                                                                                                                                                                                  94WO-US010725
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        /*tag=
/note=
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                                                                                                                 which bind to bcl-2 mRNA - breast cancer.
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83.3%;
                                                                                                                                                                                                                                                                                                                        . "3'-5'
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Pred.
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                      (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 73;
Mismatches
                                                                   for their ability to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 Other;
                                                                                                                                                                                                                                                                                                                        sequence"
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                                                                                                                              treatment
                                                     lymphoma cell
                                region (AAQ86656-
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                                                                                                                                                                                                                                                                                                                                                                                                                      therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                              of human
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RESULT 39
AAV28172/c
ID AAV28172/c
ID AAV281
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KW affini
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XX AV281
CC AAV281
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CC CONSPIC
CC Oligor
RESULT 40
AAX18693/c
ID AAX18
XX
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                AAV28155-268 represent oligonucleotides which can be purified using the method of the invention. The specification describes a matrix that comprises a support and an affinity unit that specifically and reversibly binds a target oligonucleotide, and comprises a sequence of bases having the reverse complement of a hybridising portion of the target oligonucleotide. The matrix is used for affinity purification of synthetic oligonucleotides, specifically antisense agents, for treatment of hyperproliferative diseases, for treating a non-pathogen, non-hyperproliferative disease, e.g. Alzheimer's, for modulating expression of cell surface proteins, and to inhibit a eukaryotic pathogen,
                       AAX18693 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                            Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 79; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matrix for selective separation of oligo:nucleotide - useful for, e.g. large scale purification of anti-sense agents from their deletion derivatives formed during synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity purification; antisense; bcl-2; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGGGTCGCACGCG
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                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                         BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligonucleotide; matrix; affinity unit;
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                       DNA; 17
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93.3%;
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93.3%;
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                       В₽
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                                                                                                                                                                                                                              Score 15; DB:
Pred. No. 4e+0:
1; Mismatches
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Pred. No. 4e+02;
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                                                                                                                                                                                                                                                         4e+02;
                                                                                                                                                                                                                                                                         DB 2; Length 17;
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AAX23684/c
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AC AAX236
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (i) to treat or prevent any Gibease of Lincoln (ii) to treat or prevent any Gibease, beta-thalassemia, the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bloavailability of at least 15, preferably 17-35,% The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAX18669 to AAX18799 and AAX18801 represent antisense administration. AAX18669 to AAX18799 and AAX18801 represent antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used:
(i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bloavailability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular adhesion protein; proliferation; antisense oligonucleotide; alimentary canal; transport; gastrointestinal mucosa; cancer; Alzheimer's disease; beta-thalassemia; malaria; viral infection; HIV;
Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen; probe; cellular adhesion modulator; cellular proliferation modulator;
                                                    Deletion sequence oligonucleotide 137.
                                                                                         18-JUN-1999
                                                                                                                            AAX23684;
                                                                                                                                                                AAX23684
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17
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Similarity 93.3%;
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                                                                                                                                                                standard; DNA; 17 BP
                                                                                                                                                                                                                                                                                        AGAGGGUCGCACGCG 15
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 BP; 1 A; 7 C; 5
                                                                                       (first entry
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                                                                                                                                                                                                                                                                                                                                             Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 42
ABK90271/c
ID ABK902
XX ABK902
XX ABK902
XX 21-OCT
XX 21-OCT
XX Antise
KW CAMP x
KW inflam
KW autoim
KW tumoux
XX
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                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation, and being active against a eukaryotic pathogen, a human retrovirus, a human immunodeficiency virus (HIV), or a non-human retrovirus, including influenza virus, Epstein-Barr virus, Respiratory Syncytial Virus or cytomegalovirus (CMV). The compositions enable characterization of deletion sequence oligonucleotides having related, but different nucleobase sequences, and quantification of different species of deletion sequence ("target") oligonucleotides in a mixture. Also, if the specificity of the oligonucleotide, succeedance sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sample of target deletion oligonucleotides which are labelled and hybridize with the probe oligonucleotides of the sensor arrays. Such oligonucleotides and their targets are represented in AAX23548-X23709. Oligonucleotides characterized by the method form pharmaceutical compositions that are useful for modulating cellular adhesion or
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sensor arrays which is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                             Antisense; ss; probe; Bcl-2; cell proliferative disorder; cancer; cAMP response element; bacterial infection; viral infection; inflammation; anaphylaxis; allergy; arthritis; asthma; cytostatic; autoimmune disorder; parasitic infection; virucide; hyperplasia;
                                                                                                                                                                                ABK90271;
                                                                                                                                                                                                               ABK90271 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotide present in a mixture of target deletion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 149; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compositions comprising sensor arrays made up of unique probe oligonucleotides - useful for characterizing a sample of target d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-205198/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human retrovirus; human immunodeficiency virus; non-human retrovirus;
HIV; primer; ss.
                                                                                                               Bcl-2-targeting
                                                                                                                                                 21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9911820-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reverse complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                   AGAGGGUCGCACGCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Srivatsa GS
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3, where each array comprises a unique probe oligonucleotide,
reverse complement of part of a unique target
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                describes a novel composition comprising a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00923771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US018084.
                                                                                                               antisense oligonucleotide #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The compositions form
                                                                                                                                                                                                               DNA; 17
                                                                                                                                                                                                                                                                                                                                                                             83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is not modified, the method may be performed using
                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                               Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                             4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a method for
                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cterizing a
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                0
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RESULT 43
ABQ7859/c
ID ABQ785
XX ABQ785
XX ABQ785
XX ARTise
XX ART

02-JUL-2002

sapiens

nymphoma; 1
me disease;

25-NOV-2002 ABQ78529;

(first entry)

ABQ78529 standard; DNA; 17

ВP

Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene; cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging

purging;

Antisense oligodeoxynucleotide of the human bcl-2

문 S

5

Best Loc Matches Query Match

14;

AGAGGGUCGCACGCG 15 Conservative Local

Similarity

83.3**%**; 93.3**%**;

Score 15; Pred. No. Mismatches

4e+02;

0; Gaps DB 6; Length 17

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administering a hybrid oligomer or a bcl-2 antisense oligomer and a CRB decoy oligomer; and (3) a pharmaceutical composition comprising a hybrid oligomer or a bcl-2 antisense oligomer and a CRB decoy oligomer and a carrier. The pharmaceutical composition of the invention is useful for preventing or treating cell-proliferative disorders e.g., cancer, hyperplasia or tumourigenesis and also bacterial infection, viral infection, inflammation, anaphylaxis, allergy, arthritis, asthma, autoimmune disorders and parasitic infection. The CRE decoy oligomer and bcl-2 antisense oligomer are also useful for preventing or treating hepatitis B virus infection. The hybrid oligomers and also be used for
                                                                                                                                                                                                                                                                                                                                response element (CRE) sequence and a sequence that hybridises to the bcl 2 pre-mRNA or mRNA. Also included are: (1) inhibiting the growth of cancer cells in thro, which comprises contacting the cancer cells with a hybrid oligomer or a bcl-2 antisense oligomer and a CRE decoy oligomer; (2) treating or preventing cancer in a human, which comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid oligomer comprises a cyclic AMP response element sequence and a sequence that hybridizes to the bcl-2 pre-mRNA or mRNA useful for preventing or treating cell-proliferative disorders e.g., cancer.
Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a hybrid oligomer comprising a cyclic AMP response element (CRE) sequence and a sequence that hybridises to the bcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 13; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590754/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klem RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2001; 2001US-0263244P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-2002; 2002WO-US001967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200257480-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                screening candidate transcription factors or other molecules e.g., regulatory proteins or for diagnostic assays. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENT-) GENTA INC
                                          antisense oligonucleotide
                                                                  sequence is a
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RESULT 44
ABIL54154/c
ID ABIL541
XX
ABIL541
XX
ABIL541
XX
AC ABIL541
XX
DT 12-JUI
XX
Bcl-2
XX
DE Bcl-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ঠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1995;
18-MAY-1998;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1988;
21-FEB-1992;
20-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementary to B cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is useful for inhibiting cancer cell (lymphoma or leukemia cells) growth, for increasing the sensitivity of cancer cells to cancer chemotherapeutic agents, or for inducing cancer cell death alone or in combination with any one or more cancer chemotherapeutic agents. It is also useful for reducing the bcl-2 gene expression or impairing bcl-2 protein function, for ex vivo bone marrow purging, for removing residual malignant cells from the bone marrow, for inhibiting cancer of neoplastic cell growth, and for treating autoimmune disease
                                                       25-AUG-2000; 2000US-0227970P
29-SEP-2000; 2000US-0237009P
10-NOV-2000; 2000US-00709170
                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma; hepatoma; bile duct carcinoma; choricoarcinoma; cervical cancer; testicular cancer; lung carcinoma; bladder carcinoma; melanoma; head and neck cancer; brain cancer; cytostatic; human; gene therapy;
                                                                                                                                                                          23-AUG-2001; 2001WO-US026414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bcl-2 antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL54156 standard; DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12; Col 17; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-641579/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2000;
        (GENT-) GENTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYPE-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell lymphoma/leukaemia-2; bcl-2; oncogene; antisense; lymphoma; eukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGGGUCGCACGCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorders, and for ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 1 A; 7 C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-00724426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88US-00288692.
92US-00840716.
93US-00124256.
95US-00465485.
98US-00080285.
99US-00375514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide complementary to B cell lymphoma/leukemia for inhibiting cancer cell growth, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.34;
93.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents an antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15; DB of Pred. No. 4e+0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell growth, for treations bone marrow purging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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CC antiense oligonuclectide. The present invention is directed to the use CC of bcl-2 antisense oligomers, particularly G3139 (see ABL54148), to treat CC and prevent bcl-2 related disorders. Administration at high doses results CC in significant therapeutic responses, including low toxicity, high CC tolerance and prolonged survival. Administration at high doses for short CC periods of time (less than 14 days) also provides significant therapeutic responses in the treatment of cancer. The bcl-2 antisense oligomer may CC also be used to increase the sensitivity of a subject to cancer CC therapeutics, and in combination with hormone treatment or gene therapy. CC conditions that may be treated or prevented include cancer of the CC haematopoietic system, skin, bone and soft tissue, reproductive system, contral nervous system, peripheral nervous system, kidney, lung, respiratory system, contral and alimentary canal, lymph nodes, pancreas, CC thorax, gastrointestinal and alimentary canal, lymph nodes, pancreas, CC hepatobiliary system, or cancer of unknown primary site, non-Hodgkin's CC hepatobiliary system, breast, ovarian, prostate, cervical, testicular, cancer, cancer, renal cell carcinoma, hepatoma, bile duct carcinoma, back or brain cancer, renal cell carcinoma, hepatoma, bile duct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing cancer, tumors and carcinomas, comprises administering B cell lymphoma/leukemia-2 antisense oligonucleotide at high doses for short period for time with one or more cancer
  Sequence 17 BP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Warrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 54; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is that of a B cell lymphoma/leukaemia-2 (bcl-2)
                                                   (all claimed)
                                                                     choriocarcinoma, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klem RE,
A; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fingert
C; 5
G; 4 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ξ
                                                                        carcinoma, bladder carcinoma and
  U; 0 Other;
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밁 Ş Query Match Best Local S Matches 14 15 14; _ Similarity AGAGGGUCGCACGCG AGAGGGTCGCACGCG Conservative 83.3**%**; 93.3**%**; 15 1; Mismatches Score 15; DB 6; Pred. No. 4e+02; .. Length 17; Indels 0 Gaps

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ADMIJST 45
ADMIJS 37/6
ID ADMIJS
XX ADMIJS
AC ADMIJS
AC ADMIJS
AC ADMIJS
XX ADMIS
AC AMIS
AC AMIS
AC AM
21-FEB-1992;
20-SEP-1993;
05-JUN-1995;
18-MAY-1998;
22-DEC-1998;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal tumor; colon tumor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer; bcl-2; chemotherapy; cytostatic; gene therapy;
non-hodgkin lymphoma; prostate tumor; breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADW13837
                                                                                                                                                                                                                                                                                                                              28-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6841541-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense oligodeoxymucleotide, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 17
                                                                                                                                                                                                                                                                                                                              2000US-00724425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
92US-00840716.
93US-00124256.
95US-00465485.
98US-00080285.
98US-00288692.
99US-00375514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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RESULT 46
ADZ84115/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical carrier; and increasing the sensitivity of a tumor cell to a chemotherapeutic agent. The anticode oligomers have cytostatic activity. The oligomers may be used in gene therapy to treat cancer. The method is also useful for increasing the sensitivity of a tumor cell to a chemotherapeutic agent. The types of treatable cancer include non-lodgkin's lymphoma, prostate cancer, breast cancer, gastro-intestinal cancer, or colon cancer. The anticode oligomers are useful for inhibiting growth of cancer cells or killing tumor cells. This polynucleotide sequence represents a bcl-2 oligodeoxynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for treating cancer in a leading the administration of anticode oligomers for treating to gene expressing cancer cells. The invention further comprises: a pharmaceutical composition comprising an anticode oligomer, and a
                                                                                                                                                                                                                                                                                                                                                  Brid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADZ84115 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
                                      Composition useful for enhancing the transport of nucleic acids at various sites in the alimentary canal, comprising a modified nucleic and capric acid and lauric acid or their salts.
                                                                                                                           Teng C,
                                                                                                                                                                                      01-JUL-1997;
                                                                                                                                                                                                                                                                             US6887906-B1
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             Human bcl-2 antisense oligonucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADZ84115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 12; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treating cancer, e.g. non-Hodgkin's lymphoma, prostate cancer, or breast cancer, by administering an amount of anticode oligomer for treating the
                                                                                                 WPI; 2005-321255/33.
                                                                                                                                                                                                                 01-JUL-1998;
                                                                                                                                                                                                                                                03-MAY-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYPE-) UNIV PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                     proliferation; cancer; tumor; neoplasm; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                  delivery; antisense therapy; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                        ISIS PHARM INC
                                                                                                                           Hardee G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGGGTCGCACGCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGGUCGCACGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                      97US-00886829
                                                                                                                                                                                                                   98US-00108673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ.
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bcl-2
                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Example 2; SEQ ID NO

25;

65pp; English

07-DEC-2001; 2001AT-00001924 05-DEC-2002; 2002WO-EP013791. 12-JUN-2003 WO2003047602-A1 modified_base

/*tag= a

leoxyinosine" _base= OTHER e= "OTHER= A

Any n represents deoxyuridine or

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AC CONTRACTOR OF THE PROPERTY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM36038/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thalassemia, parasite infections and viral (including retroviral) infections. The fatty acids capric and lauric acid (and their pharmaceutically acceptable salts) serve as penetration enhancers which facilitate the transport of the therapeutic nucleic acid across mucous membranes such as those of the alimentary canal, thereby increasing their alimentary bioavailability. The composition of the invention is therefore useful for the oral or rectal delivery of therapeutic nucleic acids such as antisense oligonuclectides which to date have required parenteral administration. The compositions therefore reduce the complications (e.g., the need for sterile procedures and partient hospitalization) and the concomitant expense associated with intravenous and other traumatic means of administering therapeutic nucleic acids. Sequences ADZ84098-ADZ8410 and ADZ84221 represent antisense oligonucleotides that modulate cellular proliferation which may be used in compositions of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM36038 standard; DNA; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid used in the composition of the invention is especially an antisense oligonucleotide which decreases the expression of a cellular adhesion protein or the rate of cellular proliferation, and preferably contains a 5-methyl-cytosine base or a 2'-methoxyethoxy (2'-MOE) sugar modification. Depending on the molecular target of the antisense oligonucleotide present in the composition, the compositions can be used for the treatment of cancers and tumors, Alzheimer's disease, beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system deficiency; autoimmune disorder; systemic lupus erythematosus; SLE; myasthenia gravis; immunodeficiency disorder; AIDS; malignant tumour; ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM36038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition comprising modified nucleobase or a modified sugar residue, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified nucleobase or a modified sugar residue, and cap
lauric acid or pharmaceutically acceptable salts thereo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunostimulatory CpdI/dU DNA oligonucleotide #41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kin cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mmunosuppressive; antiinflammatory; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGGUCGCACGCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 1 A; 7 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiallergic; immunopharmacological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deoxyinosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ymphoma; infectious disease; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deoxyuridine; antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14; Length 17; 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and capric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
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INTERCELL BIOMEDIZINISCHE FORSCHUNGS.

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RESULT 48
ADM35932/c
ID ADM359
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic proteins, yet do not induce the systemic production of pro-
inflammatory cytokines such as TNP-alpha and interleukin-6 (IL-6), thus
reducing the induction of potential harmful side effects. The present
invention describes compositions that are useful for preparing a
pharmaceutical composition that can activate dendritic cells, B cells,
natural killer cells and hence treat an immune system deficiency.
Purthermore, they can be used to treat various diseases including
autoimmune disorders such as systemic lupus erythematosus (SLE) and
myasthenia gravis, immunodeficiency disorders such as AIDS, malignant
tumours that cause gastric and skin cancer as well as leukaemia and
lymphoma, and various infectious diseases for example from bacteria,
viruses and protozoa. Accordingly, such compositions exhibit
dermatological, immunosuppressive, antiinflammatory, antibacterial,
                                                                          Key
modified_base
                                                                                                                                                                                                      skin cancer; leukaemia; lymphoma; infectious disease; dermatological;
immunosuppressive; antiinflammatory; antibacterial; virucide;
antiparasitic; cytostatic; antirheumatic; antiarthritic; neuroprotect
                                                                                                                                                                                                                                                           ss; immunostimulatory; deoxyinosine; deoxyuridine; antigenic; immune system deficiency; autoimmune disorder; systemic lupus erythematosus; SLE; myasthenia gravis; immunodeficiency disorder; AIDS; malignant tumour; gastric cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide, antiparasitic, cytostatic, antirheumatic, antiarthritic, neuroprotective, antimicrobial and antiallergic activities. These oligodeoxynucleotides have immunopharmacological activity and induce synergistic antigen specific immune response of an immunopotentiating cytokine. This oligonucleotide sequence is a immunostimulatory dI/dU containing ODN taken from table 1 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligodeoxynucleic acid molecules (ODNs) that contain deoxyinosine (dI) deoxyuridine (dU). Specifically, it refers to ODN molecules that encode antigenic proteins, yet do not induce the systemic production of pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an immunostimulatory oligodeoxynucleic acid molecule in the preparation of pharmaceutical composition for treating e.g. systemic lupus erythematosus, sepsis or viral infections.
                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3 Other;
                                                                                                                                                                                       antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                      DNA oligo #3 useful for induction of natural killer lytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM35932 standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide, antiparasitic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to a novel use of immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 14; Page 111; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-569024/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGGGTNGCANGNGGTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schellack C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                     antiallergic; immunopharmacological.
/mod_base= OTHER
/note= "OTHER= Any n represents deoxyuridine or
deoxyinosine"
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Egyed A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 11; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lingnau K;

 Indels

                                                                                                                                                                                                      neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thus
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This invention relates to a novel use of immunostimulatory
CC oligodeoxymucleic acid molecules (DNNs) that contain deoxyinosine (dI) or
CC deoxyuridine (dU). Specifically, it refers to DNN molecules that encode
CC antigenic protesins, yet do not induce the systemic production of pro-
CC inflammatory cytokines such as TNF-alpha and interleukin-6 (IL-6), thus
CC reducing the induction of potential harmful side effects. The present
CC invention describes compositions that are useful for preparing a
CC pharmaceutical composition that can activate dendritic cells, B cells,
CC puthermore, they can be used to treat an immune system deficiency.
CC Furthermore, they can be used to treat an immune system deficiency.
CC mysathenia gravis, immunodeficiency disorders such as AIDS, malignant
CC mysathenia gravis, immunodeficiency disorders such as AIDS, malignant
CC dermatological, immunosuppressive, antisflammatory, antibacteria,
CC viruses and protozoa. Accordingly, such compositions exhibit
CC dermatological, immunosuppressive, antisflammatory, antibacterial,
CC viruses and protozoa. Accordingly, such compositions exhibit
CC dermatological, immunosuppressive, antisflammatory, antibacterial,
CC viruses and protozoa. Accordingly, such compositions exhibit
CC dermatological, immunosuppressive, antisflammatory, antibacterial,
CC onigodeoxymucleotides have immunopharmacological activities. These
CC oligodeoxymucleotides have immunopharmacological activity and induce a
CC synergistic antigen specific immune response of an immunopotentiating
CC containing ODN of the invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an immunostimulatory oligodeoxynucleic acid molecule in the preparation of pharmaceutical composition for treating e.g. systemic lupus erythematosus, sepsis or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmidt W, Schellack C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-2001; 2001AT-00001924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003047602-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 14; Page 107; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-2002; 2002WO-EP013791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2003-569024/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERCELL BIOMEDIZINISCHE FORSCHUNGS
18 BP; 2 A; 8 C; 1 G; 4 T; 0 U; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Egyed A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lingnau
  Other;
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닭
                                                                                                                                                                             S
                                                                                                                                                                                              Query Match
Best Local S
Matches 13
                                                                       Human soft tissue sarcoma-upregulated DNA - SEQ ID 668.
                                                                                                                        ADQ17851 standard; DNA; 337
                                Homo sapiens
                                                        soft tissue
                                                                                        26-AUG-2004
                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                18
                                                                                                                                                                                                13;
                                                                                                                                                               AGAGGGTNGCANGNGGTA 1
                                                                                                                                                                              AGAGGGUCGCACGCGGUA 18
                                                       sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                Conservative
                                                                                       (first entry)
                                                                                                                                                                                                       83.3%;
                                                                                                                                                                                               2
                                                                                                                                                                                                       Score 15;
Pred. No.
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                       4e+02;
                                                                                                                                                                                                               DB 11; Length 18;
                                                                                                                                                                                                Indels
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WO2004048938-A2

26-NOV-2003; 2003WO-US038193

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RESULT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humanomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 12037
                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI91977 standard; cDNA; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 337 BP; 55 A; 98 C; 107 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which comprises obtaining a first soft tissue sample from and a normal soft tissue sample from the same or different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; SEQ ID NO 668; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                         28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                         26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                       WO200164835-A2
                                                                                                                                                                                                                     Homo sapiens.
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           Tang YT,
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                                           (HYSE-) HYSEQ INC.
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Similarity 93.3%;
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t soft tissue sample from an individual
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WPI; 200
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                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or call differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                        treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 381 BP; 87 A; 91 C; 108 G;
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 12037; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, and treating e.g. leukemia, inflammation
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  95 T; 0 U; 0 Other;
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Search completed: March 18, 2006, 18:53:35 Job time : 423.731 secs

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Similarity

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GENERAL INFORMATION: USED TOTAL
GENERAL INFORMATION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PRILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASSESEQ for Windows Version 4.0
LENGTH: 542
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                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-30493
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US-09-925-065A-30493/c
; Sequence 30493, Application US/09925065A
; Publication No. US20040181048A1
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CGTACTGCAACTCG 410
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173120
176771
                                                        100.0%; Score 14; DI
78.6%; Pred. No. 16;
tive 3; Mismatches
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2 US-11-121-086-85
2 US-11-114-798-55
2 US-10-330-773-143
2 US-11-112-908-41
2 US-11-121-086-88
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US-10-770-726-682

US-10-770-726-3547

US-10-770-726-3952

US-10-770-726-3955
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US-11-101-244-417778

US-11-101-244-658968

US-11-101-244-65907

US-11-101-244-661338

US-11-101-244-1026066

US-11-083-784-255051

US-11-083-784-65968

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US-10-995-561-13396
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US-11-145-703-1
                                                                                        DB 6; Length 542;
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                                                           Indels
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Sequence 85, Appl
Sequence 55, Appl
Sequence 41, Appl
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Sequence 42, Appl
Sequence 43, Appl
Sequence 25, Appl
Sequence 1, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 658968,
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Sequence 658968,
Sequence 659078,
Sequence 651338,
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Sequence 659666,
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Sequence 679, App
Sequence 3952, App
Sequence 3955, Ap
Sequence 112, App
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RESULT 4

US-10-932-182A-82453/c

Sequence 82453, Application US/10932182A

; Publication No. US20060046253A1

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAWURA, NORIHISA

; APPLICANT: FUJURA, TOMOKO

; APPLICANT: FUJURA, TOMOKO

; APPLICANT: FUJURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO
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APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, WUKIKO

APPLICANT: KODAMA, YUKIKO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT PILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: Patentin version 3.3

SOFTWARE: Patentin version 3.3

SOFTWARE: DAA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-162449
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US-10-932-182A-162449/c
US-10-932-182A-162449/c
Sequence 162449, Application US/10932182A
Delication No. US20060046253A1
Publication No. US20060046253A1
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FUJIMIRA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 162449
LENGTH: 25
TYPE: DIA
ORGANISM: Saccharomyces pastorianus
US-10-932-182A-162449
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US-10-932-182A-162449/c
; Sequence 162449, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
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APPLICANT: NAKAMURA, NORII
APPLICANT: KODAMA, YUKIKO
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17 GTACTGCAACTCG 5
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Pred. No.
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SEQ ID NO 1393
LENGTH: 2055
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Best Local Similarity
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·10-932-182A-1393
                                                                                                                                                      APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHLKARI, TOSHLHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
                                                                                                                   CURRENT APPLICATION NUMBER: US/10/932,182A CURRENT FILING DATE: 2004-09-02
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CURRENT FILING DATE: 2004-09-02
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CURRENT FILING DATE: 2004-09-02
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                                                                                                     NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                          APPLICANT:
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         TYPE: DNA ORGANISM: Saccharomyces pastorianus
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KODAMA, YUKIKO
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KODAMA, YUKIKO
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Pred. No.
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Pred. No.
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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11-136-527-2658
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2658
                                                                    Best Local Similarity Matches 10; Conserv
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SEQ ID NO 1393
LENGTH: 2055
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Best Local Similarity
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                                                                                                                                             -11-136-527-2658
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CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 031896-041000
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wyeth
APPLICANT: Moun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 197023
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                                                                                                                                                            LOCATION: (2885)..(2885)
OTHER INFORMATION: n is a,
                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (2885)..(288
                                                                                                                                                                                                                             ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                    ENGTH: 3002
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1472 GTACTGCAACTCG 1484
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LING DATE: 2004-09-02
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KODAMA, YUKIKO
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ASHIKARI, TOSHIHIKO
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76.9%;
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Pred. No. 1.
                                                                                       Score 13; DB 12;
Pred. No. 1.1e+02;
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Pred. No. 1.1e+02
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                                                                                                          Length 3002;
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RESULT 11
US-10-995-561-66965/c
; Sequence 66965, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
• TITLE OF INVENTION: GENETIC POLYMORPHISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-995-561-16849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16849
LENGTH: 201
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local :
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LENGTH: 12514
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Best Local (
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.GRD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
NUMBER: OS 60/599,554
PRIOR FILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
NUMBER: OS 60/599,554
PRIOR FILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
PRIOR FILING DATE: 2004-08-09
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TITLE OP INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OP INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michele Cargill APPLICANT: Hongjin Huang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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10; Conserv
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                                   Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
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76.9%;
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Pred. No. 1.5e+02;
3; Mismatches 0
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                           Mismatches
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; TITLE OF INVENTION: CARDIOVASCULAR DISORDER
TITLE OF INVENTION: DETECTION AND USES THEE
FILE REFERENCE: CLOO1559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOPTWARE: FRASISEQ for Windows Version 4.0
; SEQ ID NO 66965
; SEQ ID NO 66965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(29871)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism
US-10-995-561-13387
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US-10-995-561-66965
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US-10-995-561-13204
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Publication No. US20050272054A1
GENERAL INFORMATION:
                                        NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13204
LENGTH: 321019
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Best Local :
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Matches 10; Conservative
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                                                                                                                           APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION UNMERS: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
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ORGANISM: Homo sapiens
                        TYPE: DNA
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Local Similarity 76.9%;
es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%;
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Pred. No. 3.5e+02;
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Pred. No. 1.
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1.3e+02;
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Publication No. US20050246794A1
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Publication No. US20050245475A1
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                                                                CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
                                  PRIOR APPLICATION NUMBER: 60/502,050
                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/101,244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                     JICANT: Scaringe, Stephen
JE OF INVENTION: Functional and Hyperfunctional sirNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                          REFERENCE: 13499US
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CATION NUMBER: 60/426,137
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                   2003-09-
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76.9%;
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.4;
Pred. No. 1
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; ORGANISM: E. coli
US-10-933-982-90062
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US-11-083-784-868490
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US-09-925-065A-138336
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LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/933,982
CURRENT FILING DATE: 2004-09-03
NUMBER OF SEQ ID NOS: 224976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods of Genetic Analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Proprietary
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification and Mapping of Single ITTLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barts
                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equence 138336, Application US/09925065A
                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/250,092 FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/252,147
FILING DATE: 2000-11-20
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                       APPLICATION NUMBER: US 60/261,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jennifer
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                                                                                                                                                                US 60/289,846
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Pred. No. 1.
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Pred. No. 1
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88.6%;

Score 12.4;

DB 6;

Length 499;

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US-10-750-185-2691
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                                                                                                                                ; LENGTH; 600
; TYPE: DNA
; ORGANISM: BOVINE MMBT13844
US-10-750-185-2691
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US-11-096-568A-11706/c
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                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 2691
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Matches 10; Conserv
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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                                                                  Matches
                                                                                   Query Match
Best Local 9
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Publication No. US20050260603A1
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Best Local (
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LENGTH: 575
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CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592FUS2
                                                                                                                                                                                                                                                                                                                   APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (1)...(575)
OTHER INFORMATION: Ceres Seq. ID no. 13656404
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ORGANISM: Triticum aestivum
                                                                                     Local Similarity
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Local Similarity 71.4%;
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                                  1 CGUACUGCAACUCG 14
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CGTGCTGCAACTCG 44
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HOLM, Tom
BATES, Stephen
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71.4%;
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                                                                                   Score 12.4; DB 8; Length 600; Pred. No. 2.2e+02;
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Pred. No. 2
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APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

PILE REFERENCE: MMI1100-1

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US/10/750,623

CURRENT FILING DATE: 2003-12-31

NUMBER OF SEG ID NOS: 64922

SOFTWARE: Patentin version 3.1

SEQ ID NO 2691

I TANDAMES
RESULT 22
US-10-467-657-4195/c
; Sequence 4195, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (1)..(847)
; OTHER INFORMATION: Ceres Seq. ID no. 12379704
US-11-096-568A-20227
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US-10-750-623-2691
; Sequence 2691, Application US/10750623
; Publication No. US20050287531A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20227, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
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ORGANISM: Bovine MMBT13844
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TYPE: DNA
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Local Similarity 78.6%;
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CGTGCTGCAACTCG 44
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KERR, Richard
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71.4%;
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Pred. No. 2.3e+02;
2; Mismatches 1;
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US-10-750-185-56170/c
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US-10-750-185-56170
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Best Local
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SEQ ID NO 56170
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                                                                                                       Sequence 56170, Application US/10750623 Publication No. US20050287531A1
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NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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CURRENT FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
                            APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, SUE K. APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 9218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OFTWARE: SeqWin99, version 1.04
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                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1223
TYPE: DNA
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INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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MASIGNANI Vega
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HOLM, Tom
BATES, Stephen
ROSENFELD, David
HOLM, Tom
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KERR, Richard
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Pred. No. 2
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US-11-096-568A-19170
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; ORGANISM: Bovine
US-10-750-623-56170
                                                                                                                                                                                                                                                           US-10-504-034B-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 19170
LENGTH: 1733
TYPE: DNA
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Matches
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                                                                                                                                                                                                                 Sequence 1, Application US/10504034B Publication No. US20060040343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
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                               FILE REFERENCE: 2002.716US
CURRENT APPLICATION NUMBER: US/10/504,034B
CURRENT FILING DATE: 2004-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2005-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2750-1592PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2003-0
                                                                                                                                                            APPLICANT: Van Der Geize, Robert
APPLICANT: Van Der Meijden, Pet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 34471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/437,482
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(1733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays subsp.
                                                                                          PRICANT: Hessels, Gerda
PRICANT: Diskhuizen, Lubbert
TILE OF TRANSPORT ON: Microbial delta-1-dehydrogenation of steroids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1223
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nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                        Van Der Meijden, Peter
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2003-02-19
        2004-08-05
MBER: PCT/EP03/50025
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78.6%;
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Pred. No. 2
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Pred. No. 2
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SOFTWARE: PatentIn ver. 3.3

UMBER OF SEQ ID NOS: 10

Length 3250;

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Gaps

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APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Demnis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: Patentin version 3.1
SEQ ID NO 29862
LENGTH: 3250
                                                                                                      APPLICANT: MMI GENOMICS, INC.
APPLICANT: LORINES, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Demnis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PELING DATE: 2002-12-31
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US-10-750-185-29862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-750-185-29862/c
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Best Local Similarity
                                            SOFTWARE: PatentIN version 3.1
SEQ ID NO 29862
LENGTH: 3250
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Best Local Similarity
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29862, Application US/10750185 Publication No. US20050260603A1
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  ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1354 CGTACTGCAACACG 1341
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  19866880972249
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78.6%;
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Pred. No. 3.1e-
3; Mismatches
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APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOU-2
FILE REFERENCE: MMILIOU-2
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 29967
LENGTH: 3661
                                          ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-29967
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US-10-750-623-29967
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; ORGANISM: Bovine 19866880504081
US-10-750-185-29967
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US-10-750-185-29967
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                                                                                                                         APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF ERO ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 29967
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Publication No. US20050260603A1
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Publication No. US20050287531A1
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
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                                                                                                           ENGTH: 3661
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Local Similarity 71.4%;
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KERR, Richard
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                                                                   19866880504081
88.6%;
  Score 12.4;
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Pred. No. 3.1e+02;
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Length 3661;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X82564
DATABASE ENTRY DATE: 1996-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 17084-022003 (420C)
CURRENT APPLICATION NUMBER: US/11/082,154A
CURRENT FILING DATE: 2005-03-15
                                                               PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-30
                                                                                                       PRIOR FILING DATE: 2003-09-10
                                                                                                                         PRIOR APPLICATION NUMBER: 60/502,050
                                                                                                                                                                                                                                                                                                                                                                                                      equence 1009794,
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APPLICANT: Perez, Carl
                                                                                                                                                                                           FILE REFERENCE: 13499US
                                                                                                                                                                                                          JICANT: Marshall, William
JICANT: Scaringe, Stephen
JICANT: Scaringe, Stephen
JICANT: Scaringe, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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rroprietary
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                                         SEQ ID NOS: 1591911
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Reynolds, Angela
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Stewart, Sandra
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Leung, Josephine
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US20060024820A1
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US-11-101-244-1239747
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                                                                        TITLE OF INVENTION: Functional and Hyperfunc FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR FILING DATE: 2003-09-10
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Ablication No. US20050245475A1
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Local Similarity 75.0%;
                                                             APPLICATION NUMBER: 60/426,137
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                                                                                                                                                                                                                                INVENTION: Functional and Hyperfunctional siRNA
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Scaringe, Stephen
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Marshall, William
Scaringe, Stephen
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PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
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                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
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                      Match 85.7%; Score 12; DB 10; Length 19; Local Similarity 75.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                      INVENTION: Functional and Hyperfunctional siRNA
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US20050246794A1
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Pred. No.
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Indels
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US-11-083-784-1239747/c ; Sequence 1239747, Application US/11083784 ; Publication No. US20050245475A1
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US-11-083-784-1239747
US-10-310-914A-573268
                                                            APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 573268
                                                                                                                                                                                                                                                                          Sequence 573268, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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Best Local Similarity 75.0%;
Matches 9; Conservative
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SOFTWARE: Proprietary
SEQ ID NO 1239747
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
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APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirna
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mes 9; Conserv
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75.0%;
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Pred. No.
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US-10-521-162-32/c

Sequence 32, Application US/10521162

Sequence 32, Application US/10521162

Publication No. US20050287529A1

GENERAL INFORMATION:

APPLICANT: Brandt, Kevin S.

PITILE OF INVENTION: PROTEINS AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,

FITILE OF INVENTION: PROTEINS AND USES THEREOF

FILE REFERENCE: FC-11-PCT

CURRENT APPLICATION NUMBER: US/10/521,162

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: 60/426,601

PRIOR FILING DATE: 2003-07-17

PRIOR FILING DATE: 2003-07-17

PRIOR FILING DATE: 2003-07-17

PRIOR FILING DATE: 2003-07-17

PRIOR FILING DATE: 2003-11-15
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; LOCATION: (1)..(102)
US-10-521-162-30
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US-10-521-162-30
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                                                                                                                                             ; ORGANISM: Rhipicephalus saguineus US-10-521-162-32
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APPLICANT: Brandt, Kevin S.

TITLE OF INVENTION: FILEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES, TITLE OF INVENTION: PROTEINS AND USES THEREOF FILE REFERENCE: FC-11-PCT
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: 60/319, 402
PRIOR APPLICATION NUMBER: 60/319, 402
PRIOR PLICATION NUMBER: 60/319, 402
PRIOR PLILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/426, 601
PRIOR PRILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 50
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.2 SEQ ID NO 32
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Best Local
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                                                                                  Query Match
Best Local Similarity
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Best Local Similarity
                                                               Matches
                                                                                                                                                                                   LENGTH: 10
TYPE: DNA
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 50
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3 UACUGCAACUCG 14 : | | : | | | | | | | |
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                                                               Conservative
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                                                                                  85.7%;
75.0%;
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75.0%;
                                                             Score 12; DB b; Pred. No. 2.9e+02;
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Pred. No. 2.9e+02
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US-10-932-182A-637/c
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US-10-995-561-81478
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                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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SEQ ID NO 81478
LENGTH: 201
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local Similarity
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Publication No. US20050272054A1
GENERAL INFORMATION:
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                                                                                                                          Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND TITLE OF INVENTION: DETECTION AND THE REPRESENCE.
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/995,561 CURRENT FILING DATE: 2004-11-24
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CURRENT FILING DATE: 2004-11-24
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TYPE: DNA
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                                                   NAKAMURA, NORIHISA
KODAMA, YUKIKO
                                                                                                                                            Application US/10932182A
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ION: METHODS FOR ANALYZING GENES
                                                                                          YOSHIHIRO
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75.0%;
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75.0%;
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Pred. No.
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Pred. No.
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OF INDUSTRIAL
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RESULT 43
US-09-925-065A-746961/c
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SEQ ID NO 637
SEQ TO NO 444
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                                                                                                            PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                       CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 197023
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NUMBER OF SEQ ID NOS: 197023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICANT: ASHIKARI, TOSHIHIKO
TLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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Local Similarity 75.0%;
                                                                                         APPLICATION NUMBER: US 60/261,766
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                                                                       LING DATE: 2001-01-16
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NAKAMURA, NU.
NAKAMURA, NU.
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                                                       ICATION NUMBER: US 60/289,846
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o. US20060046253A1
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for Windows Version 4.0
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75.0%;
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Pred. No.
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Pred. No. 3
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Best Local Similarity
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US-10-521-162-33
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; ORGANISM: Homo sapiens
US-09-925-065A-746961
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              CURRENT APPLICATION NUMBER: US/10/521,162
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: 60/319,402
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/426,601
PRIOR FILING DATE: 2003-11-15
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                 US-10-521-162-35/c
                                                                                                                                                                        Sequence 35, Application US/10521162
Publication No. US20050287529A1
GENERAL INFORMATION:
APPLICANT: Brandt, Kevin S.
TITLE OF INVENTION: FILEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: FORTENIS AND USES THEREOF
FILE REFERENCE: FC-11-PCT
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APPLICANT: Brandt, Keyin S.
TITLE OF INVENTION: FLEA AND TICK OCTOPAMINE RECEPTOR NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Appropriate Publication No.
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SEQ ID
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CURRENT APPLICATION NUMBER: US/10/521,162
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: 60/319,402
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 60/426,601
PRIOR APPLICATION NUMBER: 60/426,601
PRIOR APPLICATION NUMBER: 5003-11-15
NUMBER OF SEQ ID NOS: 50
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LOCATION: (8) ...(8)
OTHER INFORMATION: n = unknown
OTHER INFORMATION: Xaa at location 2 = Tyr
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ORGANISM: Rhipicephalus saguineus
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LOCATION: (3)..(278)
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No. US20050287529A1
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75.0%;
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Pred. No. 3.9e+02;
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US-09-925-065A-53948
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CURRENT APPLICATION NUMBER: US/09/925,085A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                         Sequence 53948, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827, 135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
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Publication No. US20040181048A1
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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LOCATION: (492)..(492)
OTHER INFORMATION: n = unknown
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tes 9; Conservation
FILING DATE: 2000-11-30
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22 GTACTGCAACTC 11
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Pred. No. 4.1e+02;
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Pred. No.
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PRIOR APPLICATION NUMBER: US 60/261,766

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; ORGANISM: Homo sapiens
US-09-925-065A-53948
                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                  Sequence 940300, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-940341
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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                                   CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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                                                                              FILE REFERENCE: 108827.1
                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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CURRENT FILING DATE: 2001-08-08
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Sequence 2, Application US/10800926

Publication No. US20050032731A1

GENERAL INFORMATION:
APPLICANT: MARSHALL, WILLIAM E.

TITLE OF INVENTION: OLIGORIBONUCLECTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TITLE OF INVENTION: OLIGORIBONUCLECTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TITLE OF INVENTION: OLIGORIBONUCLECTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TITLE OF INVENTION: OLIGORIBONUCLECTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TITLE OF INVENTION: OLIGORIBONUCLECTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS
TO THE IMMINENCE OF MICROBIAL INFECTION
FILE REFERENCE: P01936USG
CURRENT FILING DATE: 2001-06-18

PRIOR APPLICATION NUMBER: 09/83,550
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/517,016
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/59,745
PRIOR FILING DATE: 1995-01-20
PRIOR APPLICATION NUMBER: 08/059,745
PRIOR FILING DATE: 1993-05-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 2
LENGTH: 14
TYPE: RNA
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                                                                                                                                                                                              PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligoribonucleotide
                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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                                                                        100.0%; Score 14; DB 8; L
100.0%; Pred. No. 3.6e+02;
. Mismatches 0;
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US-10-027-632-289193

US-10-106-698-4281

US-10-106-698-4281

US-10-106-698-42076

US-09-925-065A-31587

US-10-363-345A-31587

US-10-363-345A-31588

US-10-363-483A-31588

US-10-363-483A-31588

US-10-363-483A-31588

US-10-365A-12538

US-09-925-065A-12538

US-09-925-065A-768235

US-09-925-065A-790929

US-09-925-065A-790929

US-09-925-065A-790930

US-10-027-632-266511

US-10-027-632-266511

US-10-027-632-266511
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GENERAL INFORMATION:
GENERAL INFORMATION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT ETLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
FRIOR PRIOR SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Aspergillus nidulans
US-10-369-493-36408
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/369,493.
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 36408
LENGTH: 1786
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Best Local (
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 100.0%;
Local Similarity 78.6%;
hes 11; Conservative 3
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CGTACTGCAACTCG 141
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78.6%; I
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                                                                                           Score 14; DB 6; 1
Pred. No. 4.2e+02;
3; Mismatches 0;
                                                                                                                                            Length 1786;
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ORGANISM: Burkholderia fungorum
)-10-369-493-28056
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                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/282,122A
URRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-282-122A-12964/c
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                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/206,848
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                                                                                                                                                         APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
                                                                                                                                     APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                           FILING DATE:
                                                                                                 APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                         APPLICATION NUMBER: 60/207,727
                                                                  APPLICATION NUMBER: 60/253,625
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                                                                                    LING DATE: 2000-10-23
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                                                                                                                      LING DATE: 2000-09-09
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: Hinkle, Gregory J.
: Slater, Steven C.
: Goldman, Barry S.
: Chen, Xianfeng
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Zamudio, cur
The Cheryl
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---- Robert
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                                 60/257,931
60/267,636
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SEQ ID NO 30810
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Best Local
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-10-282-122A-12964
                                                                                                                                                                                                                                                                     equence 33109, Application US/10282122A hablication No. US20040029129A1
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APPLICANT: Hinkle, Gregory
APPLICANT: Slater, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal Similarity
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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                                                                                                                                                   Zyskind,
                                                                                                                  Wall, Daniel
Trawick, John
CATION NUMBER: US/10/282,122A
                                                               orsyth, R.
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                ON: Identification of Essential Genes in Microorganisms ELITRA.034A
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                                                                                   Robert
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2003-02-20

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US-10-437-963-61758/c
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                                                                                                                                                                                                                                                TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 61758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 61758, Application US/10437963 Publication No. US20040123343A1
                                                                                        Query Match
Best Local :
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OTHER INFORMATION: Clone ID: PAT_MRT4530_6315C.1:10-437-963-61758
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR
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PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                         ORGANISM: Oryza sativa
                                                                                                                                                                                                                    TYPE: DNA
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                                                                                      Local Similarity
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Local Similarity 78.6%;
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FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/191,078 FILING DATE: 2000-03-21
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FILING DATE: 2000-10-23
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                                 1 CGUACUGCAACUCG 14
                                                                     11; Conservative
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Barbazuk, Brad
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                                                                                    100.0%;
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                                                                                      Score 14; DB 7;
Pred. No. 4.3e+02;
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                                                                     Mismatches
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                                                                                    4.3e+02;
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                                                                                 J LENGTH: 65
J TYPE: DNA
J ORGANISM: Mus musculus
US-09-908-975-23753
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_86244C.1
US-10-437-963-87284
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US-10-437-963-87284/c
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Publication No. US20040123343A1
GENERAL INFORMATION:
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                 Query Match
Best Local Similarity
                                                                                                                                                                    SEQ ID NO 23753
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Best Local
  Matches
                                                                                                                                                                                 APPLICANT: PAIGLÉR, Simchon
TITLE OF INVENTION: OLIGONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT FILLING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILLING DATE: 2001-05-02
PRIOR FILLING DATE: 2001-05-02
PRIOR FILLING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTMARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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LOCATION: (1)..(6808)
OTHER INFORMATION: unsure at all n locations
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Barbazuk, Brad
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Conservative
                 92.9%;
76.9%;
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Pred. No. 4.4e+02;
                 Score 13; DB 3;
Pred. No. 1.5e+03;
  Mismatches
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                                     Length 65
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                                                                                                     US-10-425-115-46477
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Best Local
                                  Matches
                                                                   Query Match
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CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                               ITTLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITTLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER OF SEQ ID NOS: 204966
                                                                                                                                                      LOCATION: (1)..(472)
OTHER INFORMATION: unsure at all n locations
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                                                                                                                    OTHER INFORMATION: Clone ID: MRT4577_142392C.1
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                                                                                                                                                                                       AME/KEY: unsure
                                                                                                                                                                                                                                                          ENGTH: 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LE OF INVENTION: Rice Nucleic Acid Molecules and Othe
LE OF INVENTION: Plants and Uses Thereof for Plant I
                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                             DNA
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                                  10; Conservative
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2 GUACUGCAACUCG 14
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Cao, Yongwei
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Kovalic, Dan
Yihua
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Barbazuk, Brad
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5. US20040123343A1
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                                                    92.9%;
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Pred. No.
                                                  Score 13;
Pred. No.
                                                    1.6e+03
                                                                   DB 8;
                                  0; Indels
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                                                                   Length 472;
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; OTHER INFORMATION: Clone ID: MRT4577_79000C.1 US-10-425-115-161649
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; ORGANISM: Chicken 19866894287168_1
US-10-972-079-46310
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                                                                             Query Match
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
EQ ID NO 161649
LENGTH: 653
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·10-425-115-161649/c
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CURRENT FILING DATE: 2004-10-22
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                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 96631
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                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1)..(653)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                          ORGANISM: Zea mays
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250 GTACTGCAACTCG 238
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                                                          Similarity
CGUACUGCAACUC 13
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HOLM, Tom
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KERR, Richard
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                                        Conservative
                                                          92.9%;
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76.98;
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Pred. No. 1.6e+03
                                     Score 13; DB 8;
Pred. No. 1.6e+0:
3; Mismatches
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                                                                           Length 653;
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428 CGTACTGCAACTC 416

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; CRGANISM: CIYZA SATIVA
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96760C.1
US-10-437-963-98896
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                                                                                                                                                           US-10-437-963-84553
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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                                                                               Matches
                                                                                                                                                                                                                                                     SEQ ID NO 84553
LENGTH: 1042
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                                                                                                                  Query Match
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Publication No. US20040123343A1
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Best Local Similarity
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APPLICANT: L1, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FAPPLICATION NUMBER: US/10/437,963
CURRENT FAPPLICATION NUMBER: US/10/437,963
CURRENT FILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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OTHER INFORMATION: Clone ID: PAT_MRT4530_83779C.1
                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 838
                                                                                                Local Similarity
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                                        1 CGUACUGCAACUC 13
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Wu, Wei
Boukarov, Andrey A.
Barbazuk, Brad
CGTACTGCAACTC 1007
                                                                             Conservative
                                                                                              92.9%;
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76.91;
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                                                                                                Score 13; DB 7;
Pred. No. 1.6e+03;
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Pred. No. 1.6e+03;
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                                                                                                                  Length 1042;
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                                                                             0; Indels
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; LENGTH: 1306
; TYPE: DIA
; ORGANISM: Caenorhabditis elegans
US-10-369-493-29486
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US-10-369-493-29486
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US-10-156-761-4883
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CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
                                                                                Query Match
Best Local S
Matches 10
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROS
APPLICANT: SHIBA, TADAYOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4883
LENGTH: 1239
TYPE: DNA
ORGANISM: Streptomyces avermitilis
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Best Local Similarity 76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF INTENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERENCE: 38 -10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR DATE: 2002-02-21 PRIOR PRIOR DATE: 2003-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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PPLICANT: SAKAKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1176 GTACTGCAACTCG 1188
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                                                                                1 Similarity
10; Conserv
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HORIKAWA, HIROSHI
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. US20030119018A1
                                                                                  Conservative
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                                                                                                      Score 13; DB 6;
Pred. No. 1.6e+03;
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Pred. No. 1.6e+03;
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Best Local Similarity
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                                                                                                                           LUCATION: (1)..(1473)
-10-957-828-11
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CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/957,828
                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2004-103652 PRIOR FILING DATE: 2004-03-31
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blication No. US20050196754A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (142)..(699)
OTHER INFORMATION: 72% homologous to Escherichia coli RhsD protein,accession
OTHER INFORMATION: number X60999,Smith-Waterman Score=684.
                                                                                                                                                NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                        UMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                    »RGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: L-CYSTEINE PRODUCING MICROORGANISM AND METHOD FOR PRODUCING ITLE OF INVENTION: L-CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLICANT: Hyseq, Inc
TLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                        ID NO 11
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YAMAGUCHI, AKIHIT
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Pred. No.
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RESULT 21
US-09-815-242-6126/c
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PRIOR FILING DATE: 2000-03-21
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NAME/KEY: CDS
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ication No. US20040029129A1
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Zyskind, Jud
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Malone, Cheryl
                                                                                                                                                                                      Haselbeck, Robert
                                                             orsyth, R.
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ATION NUMBER: US/10/282,122A
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                              ON: Identification of Essential Genes in Microorgani
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io, Carlos
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76.9%;
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Pred. No. 1
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Query Match
Best Local Similarity
Matches 10; Conser
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Patent No. US20020127678A1
                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
                                                                            OTHER INFORMATION: mgo
-09-801-042-1
                                                                                                                                                                                                                                                       TITLE OF INVESTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE FILE REPERENCE: MAS/21123/280410
CURRENT EPLICATION NUMBER: US/09/801,042
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/229,329
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR PRIOR DATE: 2000-07-18
PRIOR PILING DATE: 2001-01-30
NUMBER: OF SEQ. ID. NOS: 12
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Best Local
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SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                           NAME/KEY: CDS
LOCATION: (7)..(1593)
                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                    FEATURE:
                                                                                                                                                                     ORGANISM: Escherichia coli
                                                                                                                                                                                                        ENGTH: 1720
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Local Similarity 76.9%;
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APPLICATION NUMBER: 60/191,078
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Pred. No.
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 Mismatches
                   1.6e+03;
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RESULT 25
US-10-450-763-25885/c
US-10-450-763-25885, Application US/10450763
; Publication No. US20050196754A1
                                                                                                                                                                                                                                                                                 APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND PO
FILE REPERENCE: 190CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR APPLICATION NUMBER: 09/640,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
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US-10-450-763-28629/c
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CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
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SOFTWARE: CUSTOM
SEQ ID NO 28629
LENGTH: 1732
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 25885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
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Best Local
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Publication No. US20050196754A1
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 790CIP3/US
PEATURE:
NAME/KEY: SIMILAR
LOCATION: (1005)..(343)
LOCATION: (1005)..(343)
OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
OTHER INFORMATION: structural protein, accession number AB000144, Smith-Waterman
OTHER INFORMATION: 1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME KEY: SIMILAR
LOCATION: (1005)..(343)
OTHER INFORMATION: 94% homologous to Escherichia coli K12 putative flagellin
OTHER INFORMATION: structural protein, accession number AE000144, Smith-Waterman
OTHER INFORMATION: 1100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                   LENGTH: 1919
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76.9%;
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Pred. No. 1.6e+03;
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Best Local 9
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CURRENT FILING DATE: 2001-05-23
FEATURE:
OTHER INFORMATION: MAP TO AL021808.1
OTHER INFORMATION: EXPRESSED IN HELA
OTHER INFORMATION: EXPRESSED IN PLAC
OTHER INFORMATION: EXPRESSED IN PLACE
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PRIOR FILING DATE: 2000-02-04
                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                    ID NO 4533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                          OF SEQ ID NOS: 49117
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Chen, Wensheng
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         IN HBL100, SIGNAL IN PLACENTA, SIGNAL
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Pred. No.
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2019 GTACTGCAACTCG 2007

2 GUACUGCAACUCG 14

Matches

10;

Conservative

92.9%;

Score 13; DB 9; Pred. No. 1.7e+03;

Length 2133;

Mismatches

Indels

0

Gaps

US-10-156-761-2636/c

Sequence 2636, Publication No.

2636, Application US/10156761 ton No. US20030119018A1

APPLICANT: OMURA, SATOSHI

HARUO

INFORMATION:

CURRENT FILING

URRENT APPLICATION NUMBER: US/10/156,761

ING DATE: 2002-05-29 (CATION NUMBER: JP 2001-204089

TLE OF INVENTION: NOVEL POLYNUCLEOTIDES

MASAHIRA

ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI SAKAKI, YOSHIYUKI

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RESULT 27
US-10-450-763-23995/c
Query Match
                                                                                                                                                                                                                     SEQ ID NO 23995
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Publication No.
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                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 790CIP3/US
                                                                            LOCATION: (1)..(774)
OTHER INFORMATION: 90% h
OTHER INFORMATION: Hrpa
                                                                                                                NAME/KEY: SIMILAR LOCATION: (1)..(7
                                                                                                                                                     FEATURE:
                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                          TLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
                                                                                                                                                                                                     ENGTH:
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/649,167
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US20050196754A1
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EXPRESSED
EXPRESSED
                                                                              90% homologous to Escherichia coli ATP-dependent helicase HrpA homolog,accession number D90780,Smith-Waterman Score=1183
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Pred. No. 1.6e+03;
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FETAL LIVER, SIGNAL
ADULT LIVER, SIGNAL
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LUNG, SIGNAL = 1
BRAIN, SIGNAL =
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; LOCATION: (1)..(774)
; OTHER INFORMATION: 90% homologous to Escherichia coli ATP-dependent helicase
; OTHER INFORMATION: HrpA homolog, accession number D90780, Smith-Waterman Score=1183.
US-10-450-763-25886
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 2636
LENGTH: 2559
                                                                                                                                                           Sequence 10475, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local Similarity
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Publication No. US20050196754A1
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
                                                                         APPLICANT:
                                                                                                        APPLICANT:
                                                                                                                     APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/08631 PRIOR FILING DATE: 2001-03-30
                                                        APPLICANT:
                                                                                         APPLICANT:
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PRIOR FILING DATE: 2000-08-23
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PRIOR FILING DATE: 2000-03-31
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NAME/KEY: CDS
(1)..(2559)
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NAME/KEY: SIMILAR
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                Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
                                                     Wang, Aijun
Ordonez, Nadia
                                                                                    Mannion, Jane
Clapper, Jonathan David
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Corporation
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                        92.9%; Score 13; DB 9; 76.9%; Pred. No. 1.7e+03;
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Pred. No.
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RESULT 31
US-10-154-884B-10475/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10475, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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                                         TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
CURRENT EPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
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CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 10979
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/200,779 PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-03-17
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LOCATION: (1)...(51657)
OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUMBER: US 60/200,779 FILING DATE: 2000-04-28
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Retter, Marc W.
Corixa Corporation
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76.9%;
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Pred. No. 1.8e+03;
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APPLICATION NUMBER: US 60/206,201 FILING DATE: 2000-05-22

APPLICATION NUMBER:

2000-05-01 TUMBER: US 2000-05-04

US 60/202,084

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RESULT 32
US-10-331-053-61/c
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                                                                                                Sequence 9, Application US/10398221
Publication No. US20040018514A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE
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OTHER INFORMATION: n = g, a, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(83493)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus
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ITLE OF INVENTION: Novel Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 83493
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                                                                                                                                                                                                   36317 CGTACTGCAACTC 36305
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                                                                                                                                                                                                                                                                    Conservative
ATION NUMBER: US/10/398,221
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              Listeria innocua, genome and applications 702 - \text{US}
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76.9%;
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                                                                                                                                                                                                                                                                                    Score 13;
Pred. No.
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Pred. No. 1.
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equence 1, Application US/10156761 hablication No. US20030119018A1

INFORMATION:

SATOSHI

JRRENT APPLICATION NUMBER: US/10/156,761

ON: NOVEL POLYNUCLEOTIDES

IKEDA, HARUO ISHIKAWA, JUN HORIKAWA, HIROSHI SHIBA, TADAYOSHI SAKAKI, YOSHIYUKI HATTORI, MASAHIRA

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                                                                                                                                               ; ORGANISM: Listeria innocua
US-10-398-221-2058
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                                                                                                                                                                                                                        SEQ ID NO
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                                                                       Matches
                                                                                                          Query Match
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Publication No. US20040018514A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION UNMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03
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                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 344 702 - US
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2634732 CGTÁCTGCÁÁCTC 2634744
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                                                                     Local Similarity 76.9
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                              CGUACUCCAACUC 13
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76.9%;
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76.9%;
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Pred. No.
                                                                                      Score 13; DB 7;
Pred. No. 1.4e+0;
                                                                         Mismatches
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                                                                                        1.4e+03
                                                                                                        Length 3011208;
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                                                                                                                RESULT 37
                                                                                                 US-10-843-527-74019
                                                                                                                                                                                                                                                                                                    US-10-156-761-1
             Sequence 74019, Application US/10843527
Publication No. US20050136395A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: Bric Schell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
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PRIOR FILING DATE: 2001-05-30
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OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptomyces avermitilis FEATURE: NAME/KEY: misc feature LOCATION: (4187715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                  GTACTGCAACTCG 5955043
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SAKAKI, YOSHIYUKI
HATTORI, MASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                  Score 13;
Pred. No.
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Pred. No.
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8.2e+02;
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8.2e+02;
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; ORGANISM: SARS Virus
US-10-843-527-74019
; ORGANISM: SARS Virus
US-10-843-527-163184
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; ORGANISM: SARS Virus
US-10-843-527-74993
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US-10-843-527-74993
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Best Local S
Matches 10
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CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
NUMBER OF SEQ ID NOS: 238196
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 74019
LENGTH: 25
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 74993
LENGTH: 25
                                                                       PRIOR FILING DATE: 2003-05-
NUMBER OF SEQ ID NOS: 23819
SOFTWARE: Microarray Probe
SEQ ID NO 163184
                                                                                                                                                                                                                                                                                                           Sequence 163184, Application US/10843527 Publication No. US20050136395A1
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Publication No. US20050136395A1
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Best Local (
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TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILLING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILLING DATE: 2003-05-08
PRIOR FILLING DATE: 2003-05-08
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                                                                                                                             CURRENT APPLICATION NUMBER: US/10/843,527
CURRENT FILING DATE: 2004-05-10
PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
                                                                                                                                                                                                           APPLICANT: Eric Schell
TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
FILE REFERENCE: 3602.1
                                                                                                                                                                                                                                                     APPLICANT: Michael Mittmann APPLICANT: Eric Schell
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Michael Mittmann
APPLICANT: Eric Schell
                                       TYPE:
                                                       ENGTH: 25
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71.4%;
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78.6%;
                                                                                             Sequence Listing Generator V 1.1
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Pred. No. 3.3e+03
3; Mismatches
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Pred. No. 3.3e+03;
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RESULT 42
US-10-425-115-49773/c
; Sequence 49773, Application US/10425115
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US-10-767-701-28070
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Mol
TITLE OF INVENTION: Plants and Uses Thereof For Plant I
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28070, Application US/10767701
Publication No. US20040172684A1
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/469,545
PRIOR FILING DATE: 2003-05-08
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CURRENT FILING DATE: 2004-05-10
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APPLICANT: Eric Schell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LO-767-701-28070/c
                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: SARS Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLE OF INVENTION: Methods of Genetic Analysis of SARS Virus LE REFERENCE: 3602.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
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78.6%;
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Pred. No. 3.3e+03;
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Pred. No. 3.3e+03;
3; Mismatches 1;
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Pred. No. 3
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RESULT 44
US-10-424-599-133643
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US-10-424-599-53399
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US-10-425-115-49773
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 53399
LENGTH: 229
                                                        Sequence 133643, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Publication No. US20040031072A1
GENERAL INFORMATION:
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SEQ ID NO 49773
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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TITLE OF INVENTION: Nuclaic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
PPLICANT: La Rosa Thomas J
PPLICANT: Kovalic David K
PPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                      Score 12.4;
Pred. No. 3.
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Pred. No. 3.5e+03;
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ITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement ILE REFERENCE: 38-21(53223)B

Cao Yongwei

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RESULT 46
US-10-424-599-106360
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 133643
LENGTH: 258
                                                                                                                                                                                                                           Sequence 106360, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 106360
LENGTH: 308
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Best Local Similarity
Matches 10; Conserv
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SEQ ID NO 2980
LENGTH: 285
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Best Local Similarity
                             APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: 1003-04-28
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                     APPLICANT: La ROSa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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LOCATION: (1)..(285)
OTHER INFORMATION: unsure at all n locations
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71.4%;
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71.4%;
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Pred. No. 3.5e
3; Mismatches
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Pred. No. 3
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                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_79318C.1 US-10-425-115-161997
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US-10-425-115-161997
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APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (5222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 161997

LENGTH: 322
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5)222)B
FILE REFERENCE: 38-21(5)222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATS: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 86279
LENGTH: 312
Best Local Similarity
Matches 11; Conserv
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ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_6705C.1
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                                                                                                                                                             TYPE: DNA
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78.6%;
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71.4%;
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  Score 12.4; DB 8;
Pred. No. 3.6e+03;
2; Mismatches 1;
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Pred. No. 3.5e+03;
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Pred. No. 3.5e+03;
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                                         Length 322;
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US-10-424-599-68441/c
Search completed: March 19, 2006, 07:53:06 
Job time : 2134.77 secs
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OTHER INFORMATION: Clone ID: PAT_MRT3847_96745C.1
US-10-424-599-139244
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US-10-424-599-139244/c
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JS-10-424-599-68441
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LENCTH: 331
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
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Best Local Similarity
Matches 10; Conserv
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LENGTH: 343
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Best Local Similarity
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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ITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ILE REFERENCE: 38-21(53223)B
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71.4%;
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   d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptoda
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/cgn2 6/ptodata/1/ina/5_COMB.seq:*
/cgn2 6/ptodata/1/ina/6_COMB.seq:*
/cgn2 6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2 6/ptodata/1/ina/PCTUS_COMB.seq:*
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-147054
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRIOR FILING DATE: 40/241,755
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PRIOR PR
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US-09-801-042-1/c
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                                                                   Sequence 1, Application US/09801042
Patent No. 6630332
GENERAL INFORMATION:
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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Best Local Similarity
Matches 10; Conser
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APPLICANT: RIEPING, ME APPLICANT: THIERBACH,
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US-01-062-548-19
US-01-062-548-19
US-09-252-991A-33-1
US-08-483-433-1
US-09-252-991A-3111
US-09-252-991A-7032
US-09-252-991A-7032
US-09-253-110-1269
US-09-265-315-102
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Pred. No. 3.7e+02;
3; Mismatches 0
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3418, Ap
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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for W
; SEQ ID NO 16941
; LENGTH: 21372
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16941
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CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/229,329
PRIOR FILING DATE: 2000-09-01
PRIOR REPLICATION NUMBER: DE 10 34 833.5
PRIOR REILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: DE 101 03874.7
PRIOR APPLICATION NUMBER: DE 101 03874.7
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                  Query Match
Best Local
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                                                                              Matches
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APPLICANT: MOLENAAR, DOUWE
TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF
FILE REFERENCE: MAS/21123/280410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Escherichia coli
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OTHER INFORMATION: mgo gene
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LOCATION: (7)
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RESULT 4
US-09-949-016-15868
; Sequence 15868, Application
; Patent No. 6811339
; GENERAL INFORMATION:

US/09949016

APPLICANT: VENTER, J. Craig et al.

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Matches
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TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent No. 6783961

PILE REPERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
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                                                                                                                                                                                                                                                                        09-513-999C-2299/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Drosophila melanogaster 09-270-767-27123
                                                                                                                                                                                  NPPLICANT: Dumas Milne Edwards, J.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 2000-1
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LING DATE: 2000-09
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                                                                                                                                                      Duclert, A.
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71.4%; Pred. No. 7.1
Live 3; Mismatches
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08-303-861-15
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NFORMATION FOR SEQ ID NO:
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OCATION: 23..322
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                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Palan-
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                                                                                                                                                   APPLICATION NUMBER: US/08/303,861 FILING DATE: 09-SEP-1994 CLASSIFICATION: 435
                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                                               NAME: PARK, FREDDIE K. REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                                              USA
                                   (415) 494-0792
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BYPE HERDESVIRUS TYPE
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Pred. No. 7
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RESULT 9
US-09-252-991A-79/c
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                                                                                                                        PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 79
LENOTTO: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                    Sequence 79, Application US/09252991A Patent No. 6551795
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SEQ ID NO 681
LENGTH: 399
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Best Local Similarity
Matches 11; Conserv
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 Best Local Similarity 78.6 Matches 11; Conservative
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                                  Query Match
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                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT PPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                   APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19335
                                                                               LENGTH: 435
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY: CDS
LOCATION: 13..399
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78.6%;
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Score 12.4; DB 3; Length 435; Pred. No. 8.2e+02; 2; Mismatches 1; Indels
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Pred. No. 8.1e+02;
3; Mismatches 1;
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US-09-252-991A-1326/c
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US-09-252-991A-233/c
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
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APPLICANT: MARC J. RUDENFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT EPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 1326

LENGTH: 504

TYPE: DNA

ORGANISM: Beudomonas aeruginosa
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                     SEQ ID NO 233
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                       LENGTH: 543
                                                                             Local Similarity
mes 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378
180
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CGTACTGCAATTCG 167
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71.4%;
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71.4%;
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 Mismatches

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Pred. No. 8.4e+02;
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US-09-252-991A-7705

Sequence 7705, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

RESULT 12

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LENGTH: 597
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                 Query Match
Best Local Similarity
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LENGTH: 543
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                                                                   ORGANISM: Drosophila melanogaster -09-270-767-20729
                                                                                                                 APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Fatentin Ver. 2.0
SEQ ID NO 20729
LENGTH: 597
                                                                                                                                                                                                                                                                                    Sequence 20729, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 6251'
SOFTWARE: PatentIn Ver. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Homburger et al
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CURRENT FILING DATE: 1999-02-18
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ORGANISM: Pseudomonas aeruginosa
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                                                                                                   TYPE: DNA
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     Conservative
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1998-07-27
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Pred. No. 8.5e+02;
3; Mismatches 1;
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Pred. No. 8
                   Score 12.4; DB Pred. No. 8.6e+(
   Mismatches
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                   .6e+02;
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-100
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Best Local
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APPLICANT: Marc J.
                                                                                                 Query Match
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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PRIOR APPLICATION NUMBER:
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                                                                                                                                           TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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mes 11; Conserv
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682 CGAACTGCAACTCG 669
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                               CGUACUGCAACUCG 14
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                Conservative
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1998-02-18
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78.6%;
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Pred. No. 8
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Pred. No. 8
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RESULT 17 US-09-252-991A-14097/c

Sequence 14097, Application US/09252991A Patent No. 6551795

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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 11527
LENGTH: 737
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-11527
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US-09-252-991A-94
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GENERAL INFORMATION:
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LENGTH: 726
                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 94
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-14097
                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                          PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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LENGTH: 756
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Similarity 71.4%;
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CGTACTGCAACTAG 629
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71.4%;
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Pred. No. 8.8e+02;
3; Mismatches 1
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6447
                                                                                                                                                                                                                                           APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Secritle Reference: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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; ORGANISM: Pseudomonas
US-09-252-991A-6447
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US-09-252-991A-6447/c
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5805
LENGTH: 867
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Best Local Similarity
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Best Local :
                                                                                                                                        TYPE: DNA
ORGANISM: Myxococcus xanthus
3-09-902-540-5805
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6833447
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 CGTACAGCAACTCG 715
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                                 CGUACUGCAACUCG 14
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Pred. No. 8.9e
2; Mismatches
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                                                                                  Score 12.4; DB
Pred. No. 9e+02;
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US-09-902-540-70
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ORGANISM: Myxococcus xanthus
-09-902-540-7341
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LENGTH: 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/217,883 PRIOR FILING DATE: 2000-07-10
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atent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LICANT: Hinkle, Gregory J.

LICANT: Slater, Steven C.

LICANT: Wiegand, Roger C.

LICANT: Wiegand, Roger C.

LB OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
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                                                                                                                                     Application US/09902540
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NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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BER: US 60/074,788
yxococcus xanthus Genome Sequences and Uses Thereof (15849)B
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Pred. No. 9
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; ORGANISM: Myxococcus xanthus
US-09-902-540-70
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Best Local Similarity
SEQUENCE DESCRIPTION: SEQ ID NO: 2165-
09-107-532A-2165
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CURRENT FILING DATE: 2001-07-10
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1007
                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
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MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                           FEATURE:
                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                              STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ariniello,
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                                                           NAMB/KBY:
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Pred. No. 9
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RESULT 28
US-09-252-991A-6183
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                                                                                                                                                                                                                                                ; TYPE: DNA ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-2883
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Sequence 6183, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 2883
LENGTH: 1104
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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ORGANISM: Pseudomonas aeruginosa
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Pred. No. 9.2e+02;
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Pred. No. 9.2e+02;
                                                                                                                                                                          Score 12.4; DB 3; Length 1104;
Pred. No. 9.2e+02;
2; Mismatches 1; Indels 0
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6183
LENGTH: 1137
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Sequence 7557, Application US/09252991A; Patent NO. 6551795; GENERAL INFORMATION:
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US-09-252-991A-13050
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US-09-252-991A-6183
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 13050
LENGTH: 1152
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APPLICANT: Marc J.
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CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195.136
                                                                                                                                        APPLICANT: MARC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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78.6%;
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Pred. No. 9.3e+02;
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Best Local Similarity
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Query Match
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2000-363894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                          TYPE: DNA
ORGANISM: Mycobacterium vaccae
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                                                                                                                                                                                                                                       LE REFERENCE: 14879-093001
                                                                                                                                                                                                                                                  LICANT: Kimoto, No. 68309071hiro
LE OF INVENTION: MUTANTS OF MYCOBACTERIUM VACCAE-DERIVED
LE OF INVENTION: FORMATE DEHYDROGENASE AND USES THEREOF
                                                                                                                                                                          FILING DATE:
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    J. Rubenfield et al.
    N: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
    N: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

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1998-07-27
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1999-02-18
1ER: US_60/074,788
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78.6%;
 88.6%; Score 12.4;
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Pred. No. 9
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 Length 1206;
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                     TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                          ENGTH: 1314
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FILING DATE: 1998-07-27
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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NUCLEIC ACID AND AMINO ACID
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BER: US 60/074,788
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                                                                                  88.6%;
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                                                                                     Score 12.4;
Pred. No. 9
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RESULT 35 US-09-489-039A-4444

Sequence 4444, Application US/09489039A

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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THE
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                         GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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LENGTH: 1563
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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SEQ ID NO 4444
LENGTH: 1359
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
S-09-489-039A-4444
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GENERAL INFORMATION:
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Patent No. 6551795
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/99/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
REIOR APPLICATION NUMBER: US 60/117,747
REIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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71.4%;
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Pred. No. 9.7e+02;
3; Mismatches 1;
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Pred. No. 9.5e+02;
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 252
LENGTH: 1737
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-252/c
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                                                                         ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-279
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                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 279
LENGTH: 1737
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LENGTH: 162
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Matches
                   Query Match
Best Local
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Best Local !
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FAPELICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILLING DATE: 1998-02-18
PRIOR PILLIAGINE: US/09-02-18
PRIOR PILLIAGINE: 1998-07-27
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                               TYPE: DNA
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71.4%;
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               Score 12.4; DB 3;
Pred. No. 9.8e+02;
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Pred. No. 9.8e+02;
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Pred. No. 9.7e+02;
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RESULT 42
US-09-252-991A-1375/c
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                                                     Patent No. 6551795
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Best Local
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SEQ ID NO 4152
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etent No. 6551795
                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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     TLE OF INVENTION:
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                                                                         Application US/09252991A
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 9
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Pred. No. 9
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PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-

лыкк: US 60/094,190 1998-07-27

OF SEQ ID NOS:

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1375
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LENGTH: 2262
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Best Local Similarity
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Patent No. 6551795
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CURRENT FILING DATE: 1999-02-18
PRICE APPLICATION NUMBER: US 60/074,788
CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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URRENT FILING DATE: 1999-02-18
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                                                                                     LE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
10; Conserv
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                                                                                                                           Marc J. Rubenfield et al.

VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                     107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBER: US 60/074,788
1998-02-18
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                                                                                                        AERUGINOSA FOR DIAGNOSTICS AND
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                                                                                                                                                                                                                                                                                                                                                                                                                88.6%; Score 12.4;
71.4%; Pred. No. 1
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Pred. No. 9.
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12355
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LENGTH: 2346
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: MARC J. Rubenfield et al.

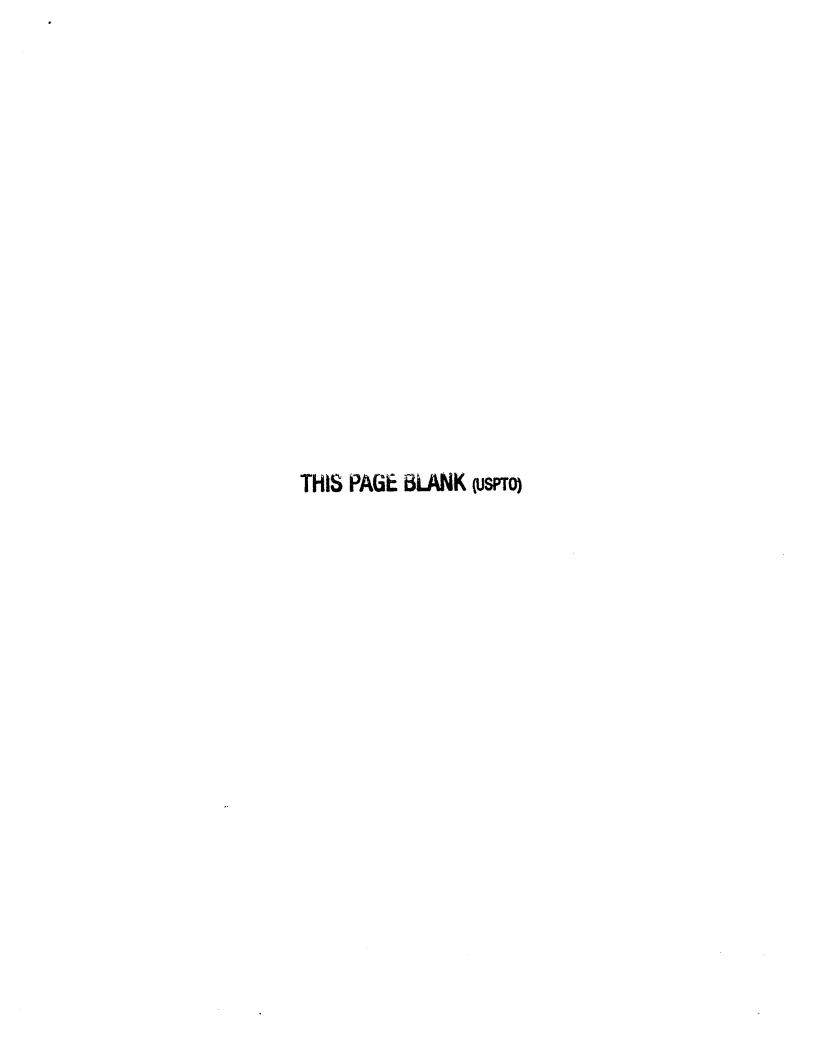
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9636, Application US/09252991A Patent No. 6551795
                                                                    Matches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: 1998-07-27
                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 107196.136
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                                                                                                                                                      LENGTH: 2346
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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ORGANISM: Pseudomonas aeruginosa
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                                 CGUACUGCAACUCG 14
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78.6%;
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                                                                  Score 12.4; DB 3;
Pred. No. 1e+03;
3; Mismatches 1;
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Pred. No. 1e+03;
2; Mismatches 1;
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Pred. No. 1e+03;
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FITTLE OF INVENTION:
FILE REFERENCE: 10715-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
PRIOR PILING DATE: 1998-07-27
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1363
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US-09-489-039A-1363
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US-09-252-991A-4456/c
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US-09-252-991A-1192
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PATENT NO. 6551795
GRMERRAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 1363
LENGTH: 2370
GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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SEQ ID NO 1192
LENGTH: 2391
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                                                                                                                                                     Sequence 4456, Application US/09252991A Patent No. 6551795
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
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71.4%;
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Pred. No. 1e+03;
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Pred. No. 1e
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Search completed: March 18, 2006, 18:39:44
Job time: 77.5769 secs
                                                                                                                                                                                                   LENGTH: 2495
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (411)..(812)
US-09-620-312D-272
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equence 272, Application US/09620312D
atent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/486,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Ma, Yunging
PPLICANT: Wang, Dunrui
PPLICANT: Wang, Zhiwei
PPLICANT: John Tillinghast
PPLICANT: John Tillinghast
TILE OF INVENTION: No. 6569662el Nucleic Acids and
ITLE OF INVENTION: Polypeptides
ILE REFERENCE: 784CIP2B
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ORGANISM: Pseudomonas aeruginosa
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Local Similarity 71.4%;
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Local Similarity 71.4%;
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Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Minimum
Maximum
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Maximum Match 100%
Listing first 1000
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Perfect score:
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seq length: 2000000000
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Copyright (c) 1993 - 2006 Biocceleration
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, N.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-CS0043-04110-464-all&t3=2000-11-04&t4=1)
                                                                                  Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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B1294829 UI-R-DK0-
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CN3066293 taf80h08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1880 Pratt Dr., Blacksburg,
Tel: 540-231-7318
Email: bmtyler@vt.edu
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Unpublished (2003)
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/clone lib=rCS0043"
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/note=rOS0043"
/note=rOS004
/no
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/lab_host="synthetic medium"
/lab_host="synthetic medium"
/clone_lib="USDA-IFAF8:Expression of Phytophthora sojae
/clone_stage="USDA-IFAF8: Expression sma"
genes during infection and propagation sma"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
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/mol_type="mRNA"
/db_xref="taxon:67593"
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
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1 (Dases 1 to 525)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."
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(mol_type="mRNA"
(db_xref="taxon:9606"
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                                                                                      Hominidae; Homo.

1 (bases 1 to 564)

1 (bases 1 to 564)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE568772 564 bp n
601342118F1 NIH_MGC_53 Homo sapiens
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                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Duke University
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Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Durham, NC 27708-1000
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Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
                                                cDNA Library Preparation: CLONTECH Laboratories, Ir cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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'strain="CC-1690 wild type mt+ 21gr"
'db_xref="taxon:3055"
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Incyte Genomics, Inc.
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Pred. No. 1.6e+03;
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1 (bases 1 to 564)

1 (bases 1 to 564)

1 (Colluta,K., Wissotski,M., Byrne,M., Stum,D., Smart,D., Smart,D., Stum, Colluta,K., Wissotski,M., Byrne,M., Stum,Colluta,K., Wissotski,M., Byrne,M., Stum,Colluta,K., Wissotski,M., Byrne,M., Stum,D., Smart,D., Stum,D., Smart,D., Stum,D., Stu
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Oryza minuta
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CZ662415
CZ662415.1 GI:70240449
GSS
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@genome.arizona.edu
Plate: 0214 row: P column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Forbes Building Room 303, Tucson, Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arizona Genomics Institute University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM_Ba0214P18.f OM_Ba Oryza minuta
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Class: BAC ends
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3' adaptor sequence:
5' -ATTCTAGAGGCGAGGCGGACGACGTG-dT (30) BN-3' (where B = A, C, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="NIH MGC_53"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgctcggcc); Site_2: SfiI
(ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and was constructed by Clontech Laboratories (Palo Alto, CA)."
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/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                           1. .564
                                                                            /tissue_type="leaves"
/lab_host="DH10B"
                                                                                                                                             /organism="Oryza minuta"
/mol_type="genomic DNA"
/db_xref="taxon:63629"
/clone="OM_Ba0214918"
                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
/clone_lib="OM_Ba"
/note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 564
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Pred. No. 1.6e+03;
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D., Muller,C., Soderlund,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑZ
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ORGANISM
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Best Local Similarity
Matches 11; Conserv
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1 (bases 1 to 587)

McCarter, J., Clifton, S., Chlapelli, B., Pape, D., Martin, J., Mylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter
at Washington University, St. Louis. Adult nematodes were harvested
from infected dogs by Dr. Prema Arasu of North Carolina State
University, Raleigh, NC (Prema Arasu@ncsu.edu) Total RNA was
isolated by Merry McLaird of Divergence, Inc., St. Louis, MO. DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dirofilaria immitis (dog heartworm nematode)
Dirofilaria immitis
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.
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587 bp mRNA linear EST 29 ke39a08.yl Dirofilaria immitis adult pAMPl vl Dirofilaria cDNA 5' similar to TR:Q9XTH8 Q9XTH8 Y37A1B.1 PROTEIN. [1]
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Fax: 314 286 1810
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Location/Qualifiers
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/morrype= maximal depression of the part of pampl. Adult nematodes were harvested from the part of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Dirofilaria immitis"
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3; Mismatches (
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Query Match Best Local Similarity

100.0%; 78.6%;

Score 14; DB 5; Pred. No. 1.6e+03;

Length 587;

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REFERENCE
AUTHORS
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CZ660542.1 GI:70234850
GSS.
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BF422183
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                                                                                               CZ660542
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      College of Genomics and Bioinformatics
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Cordonnier-Pratt MM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                         CGTACTGCAACTCG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTACTGCAACTCG 357
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                                                                         Ba0212H16.f OM_Ba Oryza
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quum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            /note=Torgan: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2:
BCORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda ZAP II. Clones to be sequenced were prepared by
                                                                                                                                                                                                                                                                                                                                                                  mass excision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cocation/Qualifiers
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                                                                                                                                                                                                                                                                                    78.6%;
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Pred. No. 1.6e+03;
3; Mismatches 0
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Psedomonas aeruginosa library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pacs2-164_4414.x3 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_4414, genomic survey sequence.
                                                                                                                                                                     University of Washington Box 352145, Seattle, WA
                                                                                                                                                                                                                                                                                                                        Spencer, D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BZ563771.1 GI:27188318
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Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza minuta
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                                                                                                                                 Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                             Genome Center
                                                                                                                                                                                                                           Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                        Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bmail: rwing@genome.arizona.edu
Plate: 0212 row: H column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 520 626 9595
Fax: 520 621 1259
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Forbes Building Room 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                               Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                          (bases 1 to 670)
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                                                                                                             craymond@u.washington.edu
/organism="Pseudomonas aeruginosa"
/mol type="genomic DNA"
/strain="2-164"
                                                         1. .670
                                                                       ocation/Qualifiers
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note="Vector: pCUGIBAC1;
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mol_type="genomic DNA"

db_xref="taxon:63629"
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BH565722/c
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CF849609/c
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Best Local Similarity
Matches 11; Conserv
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730 bp mRNA linear EST 30-OCT-psMA011xC23f USDA-IFAFS:Expression of Phytophthora sojae genes during infection and propagation_sMA Phytophthora sojae cDNA clsMA011C23 5, mKNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 711)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)
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BH565722
BH565722.1 GI:17817562
GSS.
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BOGFP49TR BOGF Brassica oleracea genomic clone BOGFP49,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTACTGCAACTCG 404
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/clone="pacs2-164_4414"
/clone lib="pacs2-164"
/clone lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                   /clone_lib="BOGF"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic_DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3712"
/clone="BOGFP49"
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Pred. No. 1.6e+03
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CW525116/c
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Tyler, B. Not Published
Unpublished (2003)
Contact: Tyler B
Tyler lab
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Seq primer: BK reverse primer
High quality sequence stop: 730.
Location/Qualifiers
                                                                                                                                                                                                                                                                              Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea; Oryzea; Oryzeae; Oryzeae;
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Tel: 540-231-7318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phytophthora sojae
Phytophthora sojae
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytophthora.
                                                                                                                                                                                         Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
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Basecalling by phred version
                                                                                                                           Purdue University 915 W. State St.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza punctata
                                   Email: sjackson@purdue.edu
                                                                    Fax: 7654967255
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                                                                                                 7654963621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="mycelium"
/cell_line="p6497"
/dev_gtage="mycelium"
/lab_host="synthetic medium"
/lab_host="synthetic medium"
/clone_lib="USDA-IFAFS:Expression_of_Phytophthora_sojae
genes_during_infection_and_propagation_sMA"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Phytophthora sojae"
|mol type="mRNA"
|db xref="taxon:67593"
|clone="sMA011C23"
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      0.020425.c.
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Query Match

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Length 759;

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BH435200
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Best Local &
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Brassica oleracea

Brassica oleracea

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              survey sequence.
BH435200
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 759)
Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis genome Res. 15 (4), 487-495 (2005)
                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brassica oleracea
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Seq primer: TAA TAC GAC TCA CTA TAG GG
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Plate: 0049 row: M o
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                                                                                                                                                                                                           Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                       Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                            Other GSSs: BOGZM10TF
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BACKWARD: CAC TCA TTA GGC ACC CCA
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                                                                                                                                                                                                                                             il: cdtown@tigr.org
  is from a_doubled haploid provided
                                                                                                                                                                                                                                                                                         301-838-0208
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4537"
/clone="OP_Ba0049M10"
/tissue_type="young leaves"
/lab_host="DH108-T1 phage resistant"
/clone_lib="OP_Ba"
                                                                                                                                                                      l. .759
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/note="Vector:
                                                                                                       mol_type="genomic DNA"
strain="TO1000DH3"
                                                                                                                                              organism="Brassica oleracea"
                                                                                                                                                                                  ocation/Qualifiers
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                                            clone_lib="BOGZ"
                                                                 clone="BOGZM10"
                                                                                  db_xref="taxon:3712"
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"Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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Pred. No. 1.6e+03
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110, genomic
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CW528167/c
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CW780591
OP_Ba0084F10.f OP_B
5', genomic survey se
CW780591
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161000 Std Brror: 0.00
Plate: 0029 row: D column: 07
Seq primer: CAC TCA TTA GGC ACC CCA
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Hatfield,J., Soderlund,C., Wing,R.
OMAP Project - Purdue University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bamail: sjackson@purdue.edu
Basecalling by phred version 0.020425.c.
from the raw sequence read by clipping wi
Bases 120-895 of the raw sequence (length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott A. Jackson Jackson Laboratory
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SanMiguel, P., Weste
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                                                                                                                                                                                                                                                                   /organism="Oryza punctata"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:453"
/clone="op_Ba0029D07"
/tissue_type="young leaves"
/lab host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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               sequence
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                              Ba Oryza punctata genomic clone OP
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                                                                                                                                                                                               Pred. No. 1.60
3; Mismatches
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                                               851 bp
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                                                                                                                                                                                                              1.6e+03
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                                                                                                                                                                                                                              DB 10;
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Kudrna,D., Muller,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A linear
genomic clone
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                                                                                                                                                                                                                            Length 776;
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                                                 linear
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COMMENT
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CW519957/c
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JOURNAL
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Best Local Similarity 78.6%;
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Oryza punctata
                                                                         Oryza punctata

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Spermatodybyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 855)

Sammiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

OMAP Project - Purdue University

Unpublished (2004)

Contact: Scott A. Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TAA TAC GAC TCA CTA TAG Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s.
Bases 36-886 of the raw sequence (length 1035) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purdue University
915 W. State St., West Lafayette,
Tel: 7654963621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A. OMAP Project - Purdue University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                     5', genomic survey sequence.
CW519957
CW519957.1 GI:53994179
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OP_Ba0023E10.f OP_Ba Oryza
5', genomic survey sequence.
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Plate: 0084
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Purdue University
915 W. State St., West Lafayette,
Tel: 7654963621
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|mol type="genomic DNA"
|db_xref="taxon:4537"
|/clone="OP_Ba0084F10"
|/tissue_type="young leaves"
|/lab_host="DH10B-T1 phage resistant"
|/clone_lib="OP_Ba"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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Pred. No. 1.6e+03;
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OP__Ba0023E10
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BF031922/c
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Bases 41-895 of the raw sequence (length 1396) were retained after
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BACKWARD: CAC TCA TTA GGC ACC CCA
INSERT Length: 161000 Std Error: 0.00
Plate: 0023 row: E column: 10
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 859)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                             CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can I
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM501 row: a column: 10
High quality sequence stop: 507.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BF031922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF031922 859 bp mRNA linear EST 10-OCT-2000 601559533F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE;3829137 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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/tissue_type="hypernephroma"
/lab_host="PH10B (TI phage-resistant)"
/clone_lib="NIH MGC_58"
/clone_Togan: kidney; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: kidney; Vector: pSfiI (ggccattatggcc);
SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="op_Ba0023E10"
/clssue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/lab_host="DH10B-T1 phage resistant"
/clone_llb="Op_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza punctata"
/mol_type="genomic DNA"
/db_xref="taxon:4537"
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                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                       clone="IMAGE:3829137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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3; Mismatches
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
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1 (bases 1 to 884)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF207946.1 GI:11101532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601862463F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082127 5',
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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    Conservative
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                                                                                                                                                                                                                                                    /clone libe NIH MGC 53"
/clone libe NIH MGC 53"
/clone Torgan: bladder; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccgctcggcc); Site 2: SfiI
(ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as cellws: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
                                                                                                                            3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGGGGGGGGATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCAGGGGGCGCGACTG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="carcinoma, cell line"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="IMAGE: 4082127"
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                     78.6%;
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                       Score 14; DB 2; Length 884; Pred. No. 1.6e+03;
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3; Mismatches
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No. 1.6e+03;
    Mismatches
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Gaps
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SOURCE

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SOURCE
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                                                                                                                       ACCESSION
VERSION
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AZ209474/c
LOCUS
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CW776517/c
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                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                643
                                                                                                                                                             AZ209474 943 bp DNA linear G
SP 0106 A2_G12_SP6B Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library Strongylocentrotus
genomic clone Plate=106 Col=24 Row=M, genomic survey
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                 Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SanMiguel, P., Westerman, R., Kim, H.,
Stum, D., Rao, K., Luo, M., Jetty, R., K
Hatfield, J., Soderlund, C., Wing, R. a
OMAP Project - Purdue University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: sjackson@purdue.edu
Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s.
Bases 39-954 of the raw sequence (length 967) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza punctata
Strongylocentrotidae; Strongylocentrotus
                                                                                                                         AZ209474.1 GI:8423220
                                                                                                                                               AZ209474
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Seq primer: TAA TAC GAC TCA CTA
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Jackson Laboratory
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Fax: 7654967255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purdue University
915 W. State St., West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
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1 (bases 1 to 916)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="OP_Ba0078M13"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OP_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Oryza punctata"

(mol_type="genomic DNA"

(mol_type="taxon:4537"

(db_ref="taxon:4537"
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Pred. No. 1.6e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 916;
                                                                                                                                                             survey sequence.
                                        Echinozoa;
                                                                                                                                                                                                    purple
                                                                                                                                                                                                                           GSS 31-AUG-2000
                                                                                                                                                                                   purpuratus
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TITLE
JOURNAL
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DN693741
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AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteidae; Gasterosteus.

1 (Dases 1 to 1195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 106 row: M column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                     Stanford Human Genome Center
Stanford University School of Medicine
Stanford Ave, Palo Alto, CA 94:
                                                                                                                                                                                                                                                     Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGX90-B12.yld-s SHGC-CGX Gasterosteus aculeatus cDNA clone CGX90-B12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGUACUGCAACUCG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A sea urchin genome project: Sequence scan, virtual map, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DN693741
DN693741.1 GI:62050365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cameron, RA, Davidson, EH, Hood, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                        Tel: 650 320 5917
Fax: 650 320 5801
                                                                                                                                                                                                                                       Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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h quality sequence stop: 943.
Location/Qualifiers
                                                                              quality sequence stop: 726
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                                                                                                                    jane@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="Plate=106 Col=24 Row=M"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 14; DB 9; Length 943; 78.6%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1195 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                             CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DN663186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 23
                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
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Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                   Bource
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteius.

[] (bases 1 to 1200)
                                                                                                                                                                                                                                                                                                                                                                                                    Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DN663186 1200 bp mRNA linear ST 29
CFW12-D08.yld-s SHGC-CFW Gasterosteus aculeatus cDNA clone
                                                                                                                                                                                                                                                Kingsley, D.M., Peichel, C., Balabahdra, S., Grimwood, J., Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
                                                                                                                   Email: jane@shgc.stanford.edu
Plate: 12
                                                                                                                                                  Tel: 650 320 5917 Fax: 650 320 5801
                                                                                                                                                                               Stanford Human Genome Center
Stanford University School of Me
975 S California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DN663186.1 GI:61983242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DN663186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CFW12-D08 5', mRNA sequence.
                                                                                                                                                                                                                                    Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGTACTGCAACTCG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGUACUGCAACUCG 14
                                                                                 quality sequence stop: |
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.openbiosystems.com/stickleback"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="Conner Creek sticklebacks, WA USA"
/organism="Gasterosteus aculeatus"
/mol.type="mRNA"
/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="mixed male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="CGX90-B12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="eyes"
                                                                   . 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14; DB 8; Length 1195;
Pred. No. 1.6e+03;
3; Mismatches 0; Indels
                                                                                                                                                                                                    of Medicine
                                                                                                   855
                                                                                                                                                                                     CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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240 CGTACTGCAACTCG 253
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Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
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CNB96-H05.yld-s SHGC-CNB Gasterosteus aculeatus cDNA clone
CNB96-H05 5', mRNA sequence.
DN738151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ceuacuecaacuce 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                              Plate: 96
                                                                                                                                                                                                                                                                 Tel: 650 320 5917
Fax: 650 320 5801
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Schmutz,J. and Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DN738151
                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tags from Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DN738151.1 GI:62115161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gasterosteidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1211
                                                                                                                            quality sequence start: 2 quality sequence stop: 790. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                      jane@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with an 54 bp linker primer containing an oligodT sequence preceeded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCTAGATCGGGGGGCGCCC(125-3'). Following second strand synthesis, CDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the CDNA sequence). A map of the Express 1 vector is a visitable at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
                                                                           organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.openbiosystems.com/stickleback"
/strain="Conner Creek sticklebacks, WA USA"
db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the Express 1 vector is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ibrary was constructed in the Express 1 plasmid vector pen Biosystems. First strand cDNA synthesis was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=\overline{\ }Vector: Express 1; Total and poly A+ RNA was solated from the indicated stickleback tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="mixed male and female"
                                                   type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _host="DH10B (T1 phage resistant)"
ne_lib="SHGC-CFW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gasterosteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 31-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and a cDNA
d vector by
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DN660653
LOCUS
                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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REFERENCE AUTHORS

COMMENT

TITLE

FEATURES

source

sex="mixed male and female"
tissue_type="skin"

clone="CEC48-A03"

WA USA"

ACCESSION VERSION

DEFINITION

SOURCE **CEYWORDS**

ORGANISM

RESULT 24 DN738151

밁

ORIGIN

Query Match Best Local

Matches

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Kingsley, D.M., Peichel, C. Schmutz, J. and Myers, R.M.
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Gasterosteus aculeatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEC48-A03.yld-s SHGC-CEC Gasterosteus aculeatus cDNA clone CEC48-A03 5', mRNA sequence.
                                                                                                                                                               High quality sequence stop: 806.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                      Stanford University School
                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford Human Genome
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                                                                                                                                                                                                                                                                                                                                                     75 S California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library was constructed in the Express 1 plasmid vector by Open Blosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCTAGATCGCGAGCGGCCCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna library construction fa q.php#8 The primary library was transformed and amplified in DHIOB (T] phage resistant) bacteria. Clones available
                                                                                                                                                                                                                                                        jane@shgc.stanford.edu
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organism="Gasterosteus aculeatus"
(mol_type="mRNA"
(strain="Conner Creek sticklebacks,
db_xref="taxon:69293"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="brain"
/dev_stage="adult"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CNB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Vector: Express 1; Total and poly A+ RNA was solated from the indicated stickleback tissue, and a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="mixed male and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 14; 78.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peichel, C., Balabahdra, S., Grimwood, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1289 bp
                                                                                                                                                                                                                                                                                                                                                                                      of Medicine
                                                                                                                                                                                                                                                                                                                                                         CA 94304, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1211;
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JOURNAL COMMENT
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AUTHORS
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AQ661032/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                            source
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                                                                                                                                                                                                                                                                                                                                       1 CGUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M. Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ661032 157 bp DNA linear GSS Z3-UN-1:
Sheared DNA-11G3.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-11G3, genomic survey sequence.
                                                                                                                                                                                 Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq_primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS.
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AQ661032.1 GI:5168800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei
                                                                                                                                                           Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/lab host="DH10B (TI phage resistant)"
/clone lib="SHGC-CEC"
/clone lib="SHGC-CEC"
/note="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Blosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceeded by a synthetic NotI site (first strand primer:
5'-GACTAGTTCTAGATCGCGACCGCCCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving junction of the form
'xxxATC' (where is ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.openbiosystems.com/stickleback"
/mol_type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
                                                                                organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 to 157)
                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 14; DB 8; Length 1289; 78.6%; Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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REFERENCE
AUTHORS
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CR555866/c
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Matches
                        Best Local Similarity
                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                             Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@kfz-heidelberg.de, sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany)
within the cDNR sequencing consortium of the German Genome Project.
This clone (DXFD469B092) is available at the RZPD in Barlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 bp mi
DKFZp469B092 rl 469 (synonym: pkid1)
DKFZp469B092-5', mRNA sequence.
CR555866
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10;
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Pongo pygmaeus mRNA (Bloecker, H., Boecher, M., Brandt, P., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR555866.1 GI:50249468
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//Clone = "Vector: pUC18; Site_1: SmaI; Constructed at The
//note="Vector: pUC18; Site_1: SmaI; Constructed at The
//note="Vector: pUC18; Site_1: SmaI; Constructed at The
//note="Vector: pUC18; Site_1: SmaI; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of mechanically
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is
described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun
sequencing projects. In Genome Sequencing: A Practical
Approach, eds. M. Vaudin and B. Barell, Oxford University
Press, 1999)."
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                                                                                                                                                                                                                                                                               /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
                                                                                                                              /clone lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                              dev_stage="adult"
lab_host="DH10B"
                                                                                                                                                                                                                                 clone="DKFZp469B092"/tissue_type="kidney"
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pred. No. 6.3e+03;
3; Mismatches 0;
Score 13; DB 7;
Pred. No. 6.4e+03;
3; Mismatches 0
                                                     DB 7; Length 205
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RESULT 29
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                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                          2 GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: d-ebbole@ramu.edu

Email: d-ebbole@ramu.edu

Chromatogram file of this sequence is available, see contact

Chromatogram file of this sequence is available, see contact

person; Best nr hit (April. 22, 2003) ref[NP 620661.1 | AV2 [South

person; Best nr hit (April. 22, 2003) ref[NP 620661.1 | AV2 [South

person; Best nr hit (April. 22, 2003) ref[NP 620661.1 | AV2 [South
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mgmk001xH17f.b pmk1 in pBluescriptII sk(-) plasmid Magnaporthe grisea cDNA clone mgmk001xH17 5', mKNA sequence.
BU640724
    CA374069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: mgmk001 row
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ebbole DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebbole, D. J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tags from the rice blast fungus, Magnaporthe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnaporthe grisea (anamorph: Pyricularia grisea)
                                                                                                            |:||:||||:||
GTACTGCAACTCG 236
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CGTACTGCAACTC 37
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                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                      /cell type="germinated conidia"
/clone lib="pmk1 in pBluescriptII sk(-) plasmid"
/note="Vector: pBluescriptSK; Site 1: EccRI; Site 2: XhoI;
/conidia germinated in hydrophobic surface membrane in 27C
for 12 hours. NN95 is a hygromycin phosphotransferase gene
replacement of the PMKI MAP kinase gene in the Guy11
strain background (Yu and Hamer. 1996. Genes & Dev.
10:2696). Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="NN95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="Mat1-1 hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002 this sequence version replaced gi:23353050
                                                                                                                                                                                                                     92.9%;
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                                                                                                                                                                                                                     Score 13; DB 5;
Pred. No. 6.4e+03;
                                                                                                                                                                                                   Mismatches
    285 bp
    mRNA
                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                        Length 255;
    linear
  EST 06-NOV-2002
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PUBMED COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CW452335
                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
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DEFINITION
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                                                     1 (bases 1 to 290)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, B., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Martienssen, R.A.
                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fsbb001f192n03k0 Sorghum methylation filtered library (LibID Sorghum bicolor genomic clone fsbb001f192n03, genomic survey
sorgnum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        648371 NCCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT16K01_A_F01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CW452335.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytogenet. Genome Ro
Contact: Rexroad CE
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Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: AGCGGATAACAATTTCACACAGGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 304 724 8340 x2129
Fax: 304 725 0351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cross_match v0.990329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3mail: crexroad@ncccwa.ars.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSDA, ARS, National Center for Cool and Cold Water Aquaculture
.1876 Leetown Road, Kearneysville, WV 25430, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:||:||||:|
CGTACTGCAACTC 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="NCCCWA lRT" /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'mol type="mRNA"
'db xref="taxon:8022"
'clone="1RT16K01_A_F01"
'tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13; DB 6;
Pred. No. 6.5e+03;
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RESULT 31
CW772355
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JOURNAL
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AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CW772355 292 bp DNA linear GSS 12-NOV-2004
OG_BBa0089B23.f OG_BBa Oryza glaberrima genomic clone OG_BBa0089B23
5', genomic survey sequence.
CW772355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: jbedell@oriongenomics.com
Plate: fsbb001f192 row: n colun
Seq primer: k Reverse
Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orion Genomics, LLC
4041 Forest Park Ave,
Tel: 314 615 6979
Fax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGUACUGCAACUC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza glaberrima (African rice)
Oryza glaberrima
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CW772355.1 GI:55712075
GSS.
                                                                                                               FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0089 row: B column: 23
Seq primer: TAA TAC GAC TCA CTA TAG
                                                                                                                                                                                                                  Porbes Building Room 303, Tucson, Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                   Arizona Genomics Institute University of Arizona
                                                                                                                                                                                                                                                                                                  Unpublished (2004)
Contact: Rod A. Wi
                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 292)
Kim, H., Yu, Y., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K.,
Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C.
                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                    Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ass: methylation filtered
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Location/Qualifiers
                                                                                                                                                                                   PRimers
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                                                                                                                                                                                                  : rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                      Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum
/mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="ATx623"
/organism="Oryza glaberrima"
/mol_type="genomic DNA"
/db_xref="taxon:4538"
/clone="OG_BBa0089B23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:4558"
clone="fsbb001f192n03"
                                                                                 Location/Qualifiers
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Pred. No. 6.5e+03;
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AUTHORS
TITLE
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VERSION
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SOURCE
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AJ578024
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Best Local Similarity
Matches 10; Conserv
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Sheader,D.L., Gensberg,K., Lyons,B.P. and Chipman,J.K.
Isolation of differentially expressed genes from contaminant
exposed European flounder by suppressive, subtractive,
hybridisation
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platichthys flesus (European flounder)
Platichthys flesus
Platichthys flesus
Platichthys flesus
Platichthys flesus
Platichthys flesus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rotinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Pleuronectidae; Platichthys.
                                                                                                                                                                 345 bp mRNA linear EST 07-DEC-2002
BY111672 RIKEN full-length enriched, 15 days embryo whole body Mus
musculus cDNA clone L330047G17 5', mRNA sequence.
BY111672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ578024 Platichthys flesus liver sexually immature Platichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Birmingham
Edgbaston Park Road, Birmingham, B15 2TT, UNITED KINGDOM.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Sheader DL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ578024.1 GI:33437855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              flesus cDNA clone BR2A6, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                       Mus musculus
                                                                                                                                               BY111672.1 GI:26222289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biosciences
                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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/lab host="DH10B T1 phage resistant"
/lab host="PG BBa"
/clone lib="PG BBa"
/mote="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Platichthys
/mol_type="mRNA"
/db_xref="taxon:8260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="sexually immature"
/clone_lib="Platichthys flesus liver sexually immature"
/note="country: Isle of Man:Port Erin"
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76.9%;
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Pred. No. 6.5e+03;
3; Mismatches 0
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••
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13; DB 1;
Pred. No. 6.5e+03;
3; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing pipeline with 384 multicapillary sequencer.
10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 345)
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                                                                                                                                                                           mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                  db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                         clone="L330047G17"
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                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
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1 (bases 1 to 364)

Brenner, E. D., Twigg, R. W., Runko, S. J., Katari, M. S., Dedhia, N. N., O'Shaughnessy, A. L., Balija, V., Martienssen, R. A., McCombie, R. W., Benfey, P., Coruzzi, G. and Stevenson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ginkgo biloba (maidenhair tree)
Ginkgo biloba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 516 367 8884
Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed tag sequences from Ginkgo female leaf (NYBG)
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ik85f03.g1 Ginkgo female leaf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $mail: mccombie@cshl.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="Ginkgo female leaf (NYBG)"
/note="Organ: leaf; Vector: :pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Stratagene ZAP Express cDNA Synthes:
The Tibrary was size-fractionated to enrich for largingerts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RIKEN full-length enriched, 15 days embryo whole body"
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'db_xref="taxon:3311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Ginkgo biloba"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13; DB 8;
Pred. No. 6.5e+03;
3; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
reptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
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                                                                                                                                                   mkNA linear EST 04-NOV-2004
phage cDNA library (root) Oryza
cDNA clone root--05-I05, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ginkgo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 08-JUN-2005
CDNA 3', mRNA
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AUTHORS
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AUTHORS
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CK749390
LOCUS
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      Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: nad03-5cs2 row: a column: 03
Seq primer: M13F.
                                                                                                                                                                                                208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn State University, University Park, PA 16802, USA Tel: 814 863 6413

Fax: 814 865 9131
                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
Contact: Claude dePamphilis or James Leebens-Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theses 1 to 367)

depamphilis.C., Carlson,J., Ma,H., Frohlich,M., Tanksley,S.,

depamphilis.C., Carlson,J., Arrington,J., Zahn,L., Kong,H.,

Leebens-Mack,J., Field,D., Arrington,J., Zahn,L., Kong,H.,

Druckenmiller,M., Landherr,L., Hu,Y., Ilut,D., Wall,K.,

Plock,S.Chiorean,S., Albert,V., Doyle,J., Miller,W.,

Oppenheimer,D., Soltis,D., Soltis,P. and Theissen,G.

Generation of ESTs from early flower buds of Nuphar advena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; basal Magnoliophyta; Nymphaeales;
Nymphaeaceae; Nuphar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuphar advena
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nad03-5cs2-a03 Nad03 Nuphar advena
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Fax: 82 31 321 6355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                              Mueller Laboratory
Penn State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK749390.1 GI:42639813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="14 days after germination"
/lab_host="R.coli SOLR"
/clone_lib="Rice root.R"
/clone_lib="Rice root.R"
/note="Vector: pBluescript SK(+); Site_1: BcoRI; Site_2:
XhoI; cDNA was inserted into landa Uni-ZAP XR vector at end with EcoRI and 3' end with XhoI site."
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/mol_type="mRNA"
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/clone="root--05-105"
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Pred. No. 6.5e+03;
3; Mismatches 0; Indels
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SOURCE
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FR0030316
LOCUS
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                                                                                                                                                                                                                                                                                                                                 COMMENT
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGUACUGCAACUC 13
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                                                                                                                                                                                                                                                            Centre, Hinxton, Cambridge, biohelpehgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation and analysis of 25 Mb of genomic DNA from the pufferfish Fugu rubripes by sequence scanning Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUN-1998) MRC Human Genome Mapping Centre, Hinxton, Cambridge, CB10 1SB, UK. Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 368)
Elgar, Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrania,Y., Williams,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostemi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontiformes; Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fugu rubripes GSS sequence, clone 077E20eC3, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brenner, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL026685.1 GI:3264028
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/clone="Vector: pBluescript SK (+/-); Site 1: EcoRI;
/note="Vector: pBluescript SK (+/-);
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
/note="Vector: pBluescript SK (+/-);
/note="Vector: pBluescr
                                                                                                      Location/Qualifiers
1. .368
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/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
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/dev_stage="<= 2.5mm"
/lab_host="SOLR"</pre>
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Pred. No. 6.5e+03;
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GSS 25-FEB-2004

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Project Resource

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CD733604/c
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 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg.1043, BARC-East, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis of mucosa
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 369)
Min,W., Lillehoj.H.S., Ashwell,C.M., Matukumalli,L.K., van
Tassel,C. and Han,J.Y.
Chicken intestinal lymphocyte EST database as a resource for the
analysis of micosal immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD733604.1 GI:32284453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone 1GAL_50F07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '' -trim_fasta. Vector identified by cross_match using options -minmatch 12 -minscore 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: hlilleho@anri.barc.usda.gov
                                                                               Similarity
GTACTGCAACTCG 5
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                                GUACUGCAACUCG 14
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h quality sequence stop: 369.
Location/Qualifiers
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                                                                                                                                                 /lab_host="EMDM10B"
/clone_lib="IGAL - Chicken Intestinal Lymphocyte"
/clone_rigan: Intestine; Vector: pCMV-SPORT6; Site_1
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site_1
Sall; Site_2: NotI; Normalized library from chicken
infected with coccidia duodenum and middle gut."
                                                                                                                                                                                                                       /tissue_type="Gut"
/cell_type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="077E20eC3"
/clone_lib="cosmid 077E20"
                                                                                                                                                                                                                                                                                              /strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="1GAL_50F07"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         row:
                                                                                                                                                                                                                                                                                                                                                                                organism="Gallus gallus"
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76.9%;
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Chicken Intestinal Lymphocyte Gallus
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Pred. No. 6.5e
3; Mismatches
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Pred. No.
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                                                           DB 6;
. 6.5e+03;
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RESULT 39

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                                                                                                                                                                                                              Sciurognathi; Muroidea; Muridae; Murinae; 1 (bases 1 to 379)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                      AI059369
UI-R-C1-ld-e-09-0-UI.sl UI-R-C1 Rattus norvegicus
UI-R-C1-ld-e-09-0-UI 3', mRNA sequence.
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                                                                                                                                                Genome Res. 6 (9), 791-806
8889548
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AI059369.1
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Populus trichocarpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI120564 376
F018P35Y Populus flower cDNA
Email: bento-soares@uiowa.edu
The sequence tag present in the cDNA
oligo-dT track served to identify it
                                               University of Iowa
375 Newton Road , 4156
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                               Contact: Soares, MB
Coordinated Laboratory
                                                                                                                                                                                discovery
                                                                                                                                                                                                                                                                                                                                          EST
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Unpublished (2001)
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Hiltonen, T., Karlsson, J.,
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                                                                                                                                                                                                   Normalization and subtraction:
                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 46 8 790 82
Fax: 46 8 245452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Royal Institute of Technology
Teknikringen 30, Stockholm S-10044,
Tel: 46 8 790 8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biotechnology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jansson, S., Nilsson, O., Sundberg, B., Sandberg, G. and Lundeberg, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rikerl@biochem.kth.se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:3694"
/tissue_type="floral_buds"
/clone_Tib="Populus_flower_cDNA_library"
/note="Organ:_flower"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Populus trichocarpa"
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Pred. No.
                                                                                                                  for Computational
                                                                                 MEBRF,
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                                                                                                                                                                    (1996)
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library Populus trichocarpa cDNA, mRNA
                                                                                 Iowa
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                                                                               City, IA
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 as a clone from the
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                                                                                                                  Genomics
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                                                                                 52242, USA
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Saliceae; Populus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
1 (bases 1 to 399)
Smith, T.P.L. Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P.L., Grosse, White, J., Cho, J., Fahrenkrug, S.C., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
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57554 MARC 2BOV Bos taurus cDNA 5',
AW425513
                                                                                                                                                                                                                                                                                                                                                                                   EST.
                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                        Bos taurus (cow)
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//ODGE TYPETOD-Pac (Pharmacia) with a modified
/notes Twector: pp773D-Pac (Pharmacia)
/notes Twector: pp7
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/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-C1"
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/db_xref="taxon:10116"
/clone="UI-R-C1-1d-e-09-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB
Pred. No. 6.6e
3; Mismatches
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, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 25-APR-2001
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BM032972
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                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                        1 (bases 1 to 402)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Teagaretshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watersteon, R. and Wilson, R., The Washington Univ. Nematode EST Project, 1999
Onther McCanner (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
BACKWARD: TOW: C COLUMN: 15
Plate: 31 TOW: C COLUMN: 15
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ascaris suum (pig roundworm)
Ascaris suum
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM032972 402 bp mRNA linear EST 05-NOV-2001 kh61e09.yl Ascaris suum female gonad GZ pAMP1 v2 Chiapelli McCarter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
VO.980904.e. Vector identified by cross_match with the -min
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
                                            Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                 The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ascaridoidea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
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The library was constructed by Brandi Chiapelli and Dr. James
McCarter at Washington University, St. Louis. The cDNA was made by
                                                                                                                                                                                         Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/lab host="DH10B"
/lab host="MARC 2BOV"
/clone_lib="MARC 2BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
/ibrary made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"
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                                                                                                                      Louis, MO
                                                                                                                         63108,
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AUTHORS
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AQ123512
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KEYWORDS
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Best Local Similarity 76.9%;
                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 403)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ123512
403 bp DNA linear GSS 22-SEP-1998
HS_3101_B1_E10_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3101 Col=19 Row=J, genomic survey
                                                                                                  High Throughput Sequencing Countversity of Washington 401 Queen Anne Avenue North, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ascott@jhsph.edu) of the School of Public; at John Hopkins University in Baltimore, MD. High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clontech. Directionally cloned into the UDG sites of pAMP1.
Dissected nematode tissues were provided by Dr. Alan Scott
(ascott@jhsph.edu) of the School of Public Hygene and Public Health
Class: BAC ends
                                   Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using Dynabead oligo-dT priming (Dynal). PCR based library using modified protocol from the SMART PCR cDNA Synthesis Kit from
                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ123512.1 GI:3500678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fomo sapiens (human)
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                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 96 (17),
                                                                          jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI; The library was constructed by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Dissected nematode tissues were provided by Dr. Alan Scott (ascott@jhsph.edu) of the School of Public Hygene and Public Health at John Hopkins University in Baltimore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Ascaris suum female gonad GZ pAMP1 v2
Chiapelli McCarter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Dissected female gonad (GZ=germinal zone,
most distal region of gonad)"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ab_host="DH10B"
                           row:
                                                                                                                                                                                                                                                                                                              human
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                                                                                                                                                                                                        Sequencing Center
                                                                                                                                                                                                                                                                                                                genome
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Pred. No. 6.6e+03;
                                                                                                                                                       Seattle,
                                                                                                                                                                                                                                      Hood
                                                                                                                                                         WA 98109, USA
                                                                                                                                                                                                                                                                                     9739-9744 (1999)
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LOCUS
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Best Local
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QGB18I02.)
QGB18I02,
BQ852614
                                                                                                                                     70
                                                                                                                                                                                                    10;
                                                  BQ852614
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed genes in 
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet) Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 bp mRNA linear EST 24-MAY-2005
BW915405 Amphioxus Branchiostoma floridae unpublished cDNA library,
neurula whole animal Branchiostoma floridae cDNA clone bbne053e07
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GUACUGCAACUCG 14
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center For Genetic Resource Information National Institute of Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu, J., Holland, L.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                      Similarity
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                                                                                                                                   CGTACTGCAACTC 82
                                                                                                                                                                   ccuacuccaacuc 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lli Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81-559-81-6855
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81-559-81-6856
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               . yg.abi Qg_ABCDI lettuce salinas Lactuca sativa cDNA clone, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CIT Approved Human Genomic Sperm Library /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones i B-Coli DH10B"
                                                                                                                                                                                                                                                                                  tissue_type="whole animal"
/dev_stage="neurula"
/dev_stage="Amphioxus Branchiostoma floridae unpublished
cDNA library, neurula whole animal"
                                                                                                                                                                                                                                                                                                                                                      /organism="Branchiostoma floridae"
|/mol_type="mRNA,"
|db_xref="taxon:7739"
|clone="bbne053e07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="genomic DNA"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .403
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76.9%;
                                                                                                                                                                                                                    76.9%;
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                                                                                                                                                                                                                  Score 13;
Pred. No.
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Pred. No. 6.6e+03;
                                                                                                                                                                                                    Mismatches
                                                  409 bp
                                                                                                                                                                                                                      6.6e+03
                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                  Length 408;
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LOCUS
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                                                                                                                                                SOURCE
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ852614.1
BST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] singleton, see http://cgpdb.ucdavis.edu/ for details.plate: QGB18 row: I column: 02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactuca sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
                                                                                                                                                               #10 bp BJ646387 Eptatretus burgeri adult hg106p18 5', mRNA sequence. BJ646387 BJ646387.1 GI:53861248 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actuca sativa
Suzuki,T., Shin-I,T., Kohara,Y. and Kasahara,M. Transcriptome analysis of hagfish leukocytes: a framework for understanding the immune system of jawless fishes
                                                            Eptatretus burgeri
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
1 (bases 1 to 410)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                              Eptatretus burgeri (inshore hagfish
                                                                                                                                                                                                                                                                                                                                                                             CGTACTGCAACTC 219
                                                                                                                                                                                                                                                                                                                                                                                                     CGUACUGCAACUC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Glone lib="QG ABCDI lettuce salinas"
/note="vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_TISSUB-germinating seeds
TAG_LIB-QG_ABCDI lettuce salinas
TAG_SEQ=TCTGTGCGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="B.coli"
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76.9%;
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Pred. No. 6.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 409;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OMAP Project
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274 GTACTGCAACTCG 262
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15236930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
                                                                                                                                                                                                                                           FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0005 row: I column: 24
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                        Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 413)

Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magmoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryze.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2004)
Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CL555282.1 GI:47633696
                                                                                                                                                                                                                                                                                                                                                                                                      Smail: rwing@genome.arizona.edu
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/dev_stage="adult"
/clone_lib="sptatretus burgeri adult"
/note="wild caught animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Eptatretus burgeri"
/mol_type="mRNA"
/db_xref="taxon:7764"
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                                                                                                                              /organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
                                                                               /clone="OB_Ba0005124"
/tissue_type="leaves"
/lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                          dev_stage="mature"
                                                                                                                                                                                                                      ocation/Qualifiers
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76.9%;
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RESULT 49
AW929623/c
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AJ679628/c
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Best Local &
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                                                                                                     AW929623 437 bp ms
EST338411 tomato flower buds 8 mm to
University Lycopersicon esculentum cI
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AJ679628
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AJ679628
Lycopersicon esculentum Lycopersicon esculentum
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Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, S.I., Finlayson, H.A. and Archibald, A.L. Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle Unpublished (2004)
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                                                      AW929623.1 GI:8105024
                                                                                          sequence.
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001779_L06"
                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="uterus"
/clone_Tib="CSECRANO4"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI;
NotI; Single pass sequencing. Normalised library
constructed from pig_uterus."
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CSEQRANO4 Sus scrofa cDNA clone C0001779_L06, mRNA
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Pred. No. 6.6e+03;
3; Mismatches 0
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Pred. No.
                                                                                                     buds 8 mm to pre-anthesis, Cornel esculentum cDNA clone cTOC9L9 5',
                (Solanum lycopersicum)
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Best Local
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                                                   source
                                                                                                                                                                                                                                                                                                                                                                             EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                    Email: bhnahm@ggbio.com, bhn
Location/Qualifiers
                                                                                                                 Yongin, Kyeonggi, K
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                Genomics and Genetics Institute, of Bioscience and Bioinformatics,
                                                                                                                                                                                                                                                  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Le
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Lazge-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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root--03-M13.gl Rice root lambda sativa (japonica cultivar-group)
                                                                                                                                                                                                                             Contact: Nahm B.H.
                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 459)
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van der Hoeven, R.S., Bezzerides, J.l., Matern, A.L., Holt, T.E., Liang, F., Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generation of ESTs
Unpublished (1999)
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Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tanksley,S.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; supplier: Tanksley; Flower buds and flowers were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="flower"
/dev_stage="buds 8mm-to-preanthesis"
/clone lib="tomato flower buds 8 mm to pre-anthesis,
Cornell University"
/organism="Oryza sativa (japonica cultivar-group)
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="TA496"
                                                   . .459
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clone="cTOC9L9"
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Pred. No. 6.6e+03;
                                                                                         bhnahm@bio.myongji.ac.kr
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phage cDNA library (root) Oryza
cDNA clone root--03-M13, mRNA
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/cultivar="Nackdong"
/db xref="taxon:39947"
/clone="root-03-M13"
/tissue_type="root"
/dev_stage="14 days after germination"
/clone_lib="Rice root lambda phage cDNA library (root)"
/clone_lib="Rice root lambda phage cDNA library (root)"
/clone_lib="Rice root lambda thi-ZAP XR vector at 5'
/note="Vector: pBluescript SK(+); Site_1: ECORI; Site_2:
/note="Vector: pBluescript SK(+); Site_1: ECORI; Site_1: ECORI; Site_2:
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Aaf33074 Human sec
Aas52489 E. coli D
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Ads49626 Bacterial
Aca25094 Prokaryot
Ads55136 Bacterial
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Aai22832 Probe #12 Aba67922 Human foe	627 11.4 81.4 173 4 628 11.4 81.4 173 4	10 AAD54223 Aad54223 St. 4 AAI98929 Aai98929 Hum	554 12 85.7 555 12 85.7
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11-MAY-1993;
20-JAN-1995;
18-AUG-1995;
29-OCT-1996;
17-NOV-1998;
18-JUN-2001;
                                                                                                         15-MAR-2004;
                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                  Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial immunomodulatory CpG oligoribonucleotide, SEQ ID NO:2
                                                                                                                                                                US2005032731-A1
                                                                                                                                                                                                                                                                                                                                                         Immune modulation; immune stimulation; bacterial infection; infection; endotoxic shock; antibacterial; antimicrobial; immunomodulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADW79935 standard; RNA;
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93US-00059745.
95US-00376175.
95US-00517016.
96US-00739264.
98US-00193653.
2001US-00883550.
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/note= "CpG dimucleotide"
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Aacn33174 Mutated O
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Adw21810 Rat hepat
Abz38826 N. gonor
Aaz53604 Neisseria
Addh28934 Human chr
Add63275 Transcrip
Adx12269 Plant ful
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The invention relates to a composition for modulating and/or stimulating comprising bacterial oligoribonuclectides (ORN) with a molecular weight of less than 10 kD. The bacterial ORNs are preferably ADW79934-ADW79936, contain CpG motifs and are resistant to CR when they colonize animals. The immune systems of animals have co-evolved CC when they colonize animals. The immune systems of animals have co-evolved CC when they colonize animals. The immune systems of animals have co-evolved CC invention also relates to a method for the preparation of the bacteria. The CC invention also relates to a method for the preparation of the bacterial CC ORNs by subjecting bacteria to one or more periods of stress, separating the ornewe substances with a molecular weight of more that 10 kD; and a cc method of using the filtrate to modulate/stimulate the immune system of animals to withstand microbial infection. The composition and methods cof the invention are useful for modulating and/or stimulating the limmune system of system of animals (including humans, poultry and livestock), particularly cto withstand microbial infections or the onset of endotwic shock. The parentally, and may also be administered as an adjuvant for oral or compositions may be used to extend the viability of monocytes, thereby improving their capainst ear, nose and vaginal infections. They may further be cability to mature into macrophages to fight infections. They may further be cability to mature into macrophages to fight infections. The composition of the invention contains tows released by either harmless or pathogenic containing them are non-toxic. The present sequence represent a conjugations of the inventions of the inventions. They may further be compositions of the inventions of the inventions of the inventions. They may further be composited to be compositions of the inventions of the inventions. They may further be conjugated to the prevent them from the prevent them are non-toxic. The prevent sequence represents a conjugate of the inventions 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition for modulating and/or stimulating immune system of animal useful for withstanding microbial infections and lethality of endotoxic shock, comprises low molecular weight oligoribonucleotide from bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 2; 17pp; English.
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Sequence 14 BP; 3 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate;

phosphorus; photosynthesis;

lignin; galactomannan;

Bacterial 02-DEC-2004 ADS60734;

polynucleotide #12721.

(first entry)

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RESULT 3
ADS49626/c
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                                                                                                                                                                                                                                                                                                                                                                                         comprising the recombinant DNA construct and a method of producing a comprising the recombinant DNA construct and a method of producing a companion of control of producing and transformed plant is a crop plant such as maize or soybean. The method of producing a transformed plant convergence of producing a transformed plant with the recombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with tolerance to plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polynucleotide used in the properties.
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a
 Bacterial polynucleotide #4369
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                                  02-DEC-2004
                                                                   ADS49626;
                                                                                                   ADS49626 standard; cDNA; 1981 BP
                                                                                                                                                                                                                                                                                                                Sequence 1786 BP; 374 A; 597 C; 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microbial source. The invention also relates to a transformed
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RESULT 4 ACA25094/c

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CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant CC such as maize or soybean. The method of producing a transformed plant CC having an improved property comprises transformed plant with the CC recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant, where the CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or CC content, improved yield by modification of arbohydrate, nitrogen or CC condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polynucleotide used in CC production. This sequence represents a bacterial polynucleotide used in CC condition, improved plant growth and development under at least one stress condition, part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                 Query Match
Best Local S
Matches 11
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                                                                                                                                                            Sequence 1981 BP; 448 A; 584 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter functional in a plant cell, where the promoter is positic provide for expression of a polynucleotide encoding a polypeptide
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homologous recombination; seed oil yield; protein yield; carbohydrate;
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ACA25094 standard; DNA; 1986 BP.

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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC (1) a vector comprising a promoter operably linked to the nucleic acid (2) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated CC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC polypeptide or its fragment whose expression is inhibited by the antisense CC antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular CC proliferation or the activity of a gene in an operon required for CC the gene product or that has an activity against a biological pathway CC required for proliferation, or that inhibits cellular proliferation; (8) cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an CC compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of collection of the strains; or (13) identifying the target of a compound that inhibits the collection of identifying the strains. The antisense nucleic acids are useful for identifying the capable of a compound that inhibits the collection of the strains or the strains of the strains of the collection of the strains.
                       identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at free who intrompt, which into account for the printed or account of the printed or the printed specification.
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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drug design;
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                  The invention relates to a recombinant DNA construct comprising a comproter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a comprosising the recombinant DNA construct and a method of producing a crop plant comprising the recombinant DNA construct and a method of producing a crop plant comprising an improved property. The plant is a crop plant comprising an improved property comprises transformed plant with the crecombinant DNA construct and growing the transformed plant, where the composition of producing a transformed plant the crop plant comprises transformed plant with the crecombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with comproved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition improved plant growth and development under at least one stress condition.
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HINKLE
SLATER
CHEN X.
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polynucleotide; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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5.5e+02;
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This sequence represents a bacterial polynucleotide used

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        The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the polypeptide; (7) identifying a gene in an operon required for proliferation or the activity of a gene in an operon required for required for that has an activity against a biological pathway required for proliferation, or that his an activity against a biological pathway in which a proliferation required gene or its gene product lies pathway in which a proliferation required gene product lies
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the scope of the invention. Note: The sequence data for this patent not form part of the printed specification but was obtained in elect format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the scope of the not form part of
                                                                                                                                                                                                                                                                              Claim 14; SEQ ID NO 33109; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prokaryotic essential gene #26896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACA45239;
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Trawick JD,
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Carr GJ,
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Pred. No. 5.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Forsyth
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Xu HH;
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Query Match Best Local Similarity

92.9**%**; 76.9**%**;

Score 13; Pred. No.

DB 13; 1.5e+03;

Length 21

Sequence 21

BP; 6 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

The invention relates to a polynucleotide comprising an RNA sequence. The polynucleotides, vector, libraries, and method are useful in lowering the amount of RNA and/or protein production in cells used in drug development process. The present sequence represents a knock-down target sequence.

New knockdown sequences, useful in lowering the amount of RNA and/or protein production in cells used in drug development process.

Claim 11;

SEQ ID NO 9430; 402pp; English.

Matches

Conservative

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Mismatches

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Best Local
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Griffioen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K. pneumoniae or P. aeruginosa. The present sequence is one of prokaryotic essential genes. Note: The sequence data for this prot form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/nub/wwb14.bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for proliferation of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2460 BP; 556 A; 704 C; 776 G; 424 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium
                                                                                                                                                                   WPI; 2004-775940/76.
                                                                                                                                                                                                                                                                                24-APR-2003; 2003WO-BP004362
                                                                                                                                                                                                                                                                                                            24-APR-2003; 2003WO-EP004362.
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                                                                                                                                                                                                                                                                                                                                                                     WO2004094636-A1
                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                          ds; RNA production; protein production; drug development;
knock-down target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADU44189 standard; DNA;
                                                                                                                                                                                                                                       (GALA-) GALAPAGOS GENOMICS NV. (VSCH/) VAN DER SCHUEREN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                         Lambrecht MJY,
S, Bergs CJL;
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                                                                                                                                                                                                       cc messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcriptome. Where the (sub-)transcriptome comprises several cc oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, composition or more messenger RNA splice variants. The coligonuclectide libraries are useful for detecting mRNAs from a color of coligonuclectide libraries are useful for detecting mRNAs from a color of coligonuclectide libraries are useful for detecting mRNAs from a color of color of the sequence and in color of color o
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Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002
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02-MAY-2001; 2001US-0287724P
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           Conservative
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                                       92.9%;
76.9%;
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Score 13; DB 6;
Pred. No. 1.7e+03;
3; Mismatches 0
                                                                                                                                                        10 G; 15 T;
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                                                                                                                                                        0 U; 0 Other;
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                                                                              Length 65;
   Indels
   0
   Gaps
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14

N

GUACUGCAACUCG 14

Best Loc Matches

Local

Similarity 10; Conser

Conservative

92.9%;

Score 13; Pred. No.

ed. No. 1.7 Mismatches

1.7e+03; DB 8;

Length 100

0

0

Gaps

0

RESULT

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RESULT 9
ACD687/69/c
ID ACD687/
XX ACD687/
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PF 17-MAY
XX INWGB-
PA (MWGB-
PA WPI; 2)
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                                                                                                   complementary to, a segment of an open reading frame (orf) of Escherichia (coli K12. The blochip is used for specific detection of gene expression (coli K12. The blochip is used for specific detection of gene expression (coli K12 and for determining the gene expression pattern, e.g. for (coli K12 and for determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The colichip provides as comprehensive as possible detection of the K12 and its mutants or comparison of gene expression between K12 and its mutants or cother E. coli strains in a single experiment. Apart from qualitative and comparison of gene expression between K12 and its mutants or cother E. coli strains in a single experiment. Apart from qualitative and contains in grobe expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free containtion in probe length and ensures high purity (and thus selectivity, cand reproducibility), also synthetic probes are generally containtion of probes are generally containtion of probes are generally containtied of probes are generally in the invantion.
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       Sequence 100 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 17; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression
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                                                                                       invention
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|:||:|||:||
GTACTGCAACTCG 43
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           29
       A; 28 C;
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           29
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       14 T; 0 U; 0 Other;
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ACD68770/c
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which B. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other B. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility), also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD66731 to ACD66731 to appreciate the probes are generally shorter than probes of the probes used with the blochip described and the second appreciation of probes are generally shorter than probes of the probes used with the blochip described and the probes of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-80 Dasee, and programmer of at least 20 bases identified includes a segment of an open reading frame (orf) of Escherichi complementary to, a segment of an open reading frame (orf) of Escherichi complementary to, a segment of an open reading frame (orf) of gene expression coli K12. The blochip is used for specific detection of gene expression coli K12. The blochip is used for specific detection of gene expression pattern, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences 30-80 bases, are prepared ex situ from synthetic oligonucleotides and least one includes a segment of at least 20 bases identical with, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 BP; 29 A; 23 C; 34 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 17; 2004pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochip containing probes complementary with open reading frames in Escherichia coli Kl2, useful for detecting gene expression and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001; 2001EP-00112179
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08-FEB-2001
                                                       AAC61183;
                                                                                                            AAC61183 standard; DNA; 1197
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                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                     2 GUACUGCAACUCG 14
                                                                                                                                                                                                                                                   GTACTGCAACTCG 40
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                                                                                                                                                                                                                                                                                                                                                                Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                           92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                        Score 13;
Pred. No.
                                                                                                            ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                        DB 8; 1
                                                                                                                                                                                                                                                                                                                                                                                                               Length 100
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                                                                                                                                                                                                                                                                                                                                                             Gaps
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Matches
                                                                     Query Match
Best Local (
                                                                                                                                                                                                              This invention relates to a gene encoding a formate dehydrogenase from Hyphomicrobium sp. A transformant containing the new gene is used for the preparation of formate dehydrogenase of high specific activity, low Michaelis constant (Km) value against formic acid and NAD+, high temperature stability and high pH stability. The present sequence
                                                                                                                                           Sequence 1197 BP; 290 A; 350 C; 323 G;
                                                                                                                                                                                   Michaelis constant (Km) value against formic temperature stability and high pH stability. represents the gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                      New Hyphomicrobium sp. formate dehydrogenase gene for producing formate dehydrogenase of high specific activity, high temperature stability and high pH stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Formate dehydrogenase nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 5-6; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY85650
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                                                                        Similarity
CGUACUGCAACUC 13
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00052548.
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                                                                     92.9%;
76.9%;
                                               ω
•
                                                                     Score 13;
Pred. No.
                                                                                                                                           234 T; 0 U; 0 Other;
                                                                        2e+03;
                                                                                              DB 3;
                                                                                         Length 1197;
                                               Indels
                                               0;
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Recombinant DNA construct; transformed problem tolerance; heat tolerance; drought pathogen tolerance; pest tolerance; plan
                                                                                                                                                                                                                                                                                                                                                                                                        ADS51056 standard; cDNA; 1306 BP
18-DEC-2003
                                    US2003233675-A1
                                                                            Bacteria.
                                                                                                                                    nitrogen;
                                                                                                                                                     cell cycle pathway modification; plant homologous recombination; seed oil yiel
                                                                                                                                                                                                                                                                                 Bacterial polynucleotide #5799.
                                                                                                                                                                                                                                                                                                                         02-DEC-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 CGTACTGCAACTC 443
                                                                                                                                      phosphorus;
                                                                                                                                                           yield;
                                                                                                                                                                                                    plant disease resistance;
                                                                                                                                      lignin;
                                                                                                                                                                                                                                        plant; improved
                                                                                                                                                                            growth regulator,
                                                                                                                                                       protein yield; carbohydrate;
                                                                                                                                                                                                                   property;
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(CAOY/) CAO Y.

20-FEB-2003; 2003US-00369493 21-FEB-2002; 2002US-0360039P

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ADR85906/c
ID ADR859
XX
AC ADR859
XX
DT 04-NOV
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ASPERG
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Fungic
KW Fungic
KW drug s
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OS Asperg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant DNA construct comprising a CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant having an improved property. The plant is a crop plant CC such as maize or soybean. The method of producing a transformed plant are combinant DNA construct and a method of producing a recombinant DNA construct and growing the transformed plant, where the CC polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or CC content, improved yield by modification of photosynthesis or by cc providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polynucleotide used in the scope of the printed specification but was obtained in electronic format from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
 17-JAN-2003; 2003US-0441281P
                                                                                                                                                Aspergillus fumigatus
                                                                                                                                                                                                                                        Aspergillus
                                                                                                                                                                                                                                                                                 04-NOV-2004
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(SLAT/)
(CHEN/)
(GOLD/)
                                    16-JAN-2004; 2004WO-US001099
                                                                                                                                                                                                    Fungicide;
                                                                                                                                                                                                                                                                                                                                                        ADR85906 standard; DNA; 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1306 BP; 392 A; 296 C; 253 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 29486; 122pp; English.
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SLATER
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTACTGCAACTC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGUACUGCAACUC 13
                                                                                                                                                                                    Aspergillus fumigatus infection; Farmer's lung disease; ning; ds.
                                                                                                                                                                                                                                        fumigatus essential gene open reading frame #543.
                                                                                                                                                                                                                                                                               (first entry)
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76.9%;
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Pred. No. 2e+0
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 1306;
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating invasive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be used in various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The present sequence represents an Aspergillus fumigatus essential gene open reading frame, used during diagnosis and drug development in the invention. These genes share a high degree of sequence conservation with known essential genes of candida albicans. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS73079 standard; cDNA; 1359
                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #8883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 2543; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal infections, such as Farmer's lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; ADR86493.
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(ELIT-) ELITRA CANADA LTD.
                                                            2001-639362/73
DB; ABG08892.
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                                                                                                                                                                                                              HYSEQ INC.
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                                                                                                                                                  Liu C,
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76.9%;
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Pred. No. 2e+0
3; Mismatches
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New isolated polynucleotide and encoded polypeptides, useful

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding semicones of the invention Note. The segmence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, for responsible for biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fungicide; Aspergillus fumigatus infection; Farmer's lung disease; drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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New purified or isolated encoding a gene product,
                                                                                            P-PSDB;
                                                                                                                                                                                   Jiang B,
                                                                                                                                                                                                                                                                                                                                      17-JAN-2003; 2003US-0441281P
13-JUN-2003; 2003US-0478196P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus fumigatus essential gene with introns #543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004067709-A2
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                                                                                                                                                                                                                                                   (BLIT-)
                                                                                                                                                                                                                                                                                   (ELIT-)
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                                                                                                2004-594200/57
DB; ADR86493.
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                                                                                                                                                                                                                                            ELITRA PHARM INC.
ELITRA CANADA LTD.
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                                                                                                                                                                                   Hu W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful
                                                                                                                                                                                   Lemieux S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.9%;
   Aspergillus fumigatus nucleic acid molecule useful for diagnosing and/or treating invas
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Pred. No.
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2e+03;
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RESULT 16
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gastrointestinal; solid tumour; rheumatoid arti
diabetic retinopathy; myocardial angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  essential gene sequence containing all introns, used during diagnosis and drug development in the invention. These genes share a high degree of sequence conservation with known essential genes of candida albicans. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in various drug discovery purposes, such as expression of the recombinant protein, hybridization assay and construction of nucleic acid arrays. The present sequence represents an Aspergillus fumigatus essential gene semisoro contributor of increases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating invasive Appergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be used in various drug discovery purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2000; 2000WO-US014928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; cytostatic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF33074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF33074 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI
(ROSE/) ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                                             Komatsoulis
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; anti-ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease
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<u>,,</u>

Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating diseases such as tumors, rheumatoid arthritis, psoriasis and diabetic retinopathy.

WPI; 2001-071280/08 P-PSDB; AAB64703.

Claim 1; Page 452; 520pp; English.

The polymucleotide sequences given in AAF33037 to AAF33085 encode the human secreted proteins given in AAB64666 to AAB64714. AAB64715 to AAB64771 represent human secreted polypeptide sequences and proteins

given

polypeptide en in the exc

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AAS52489/c

ID AAS52489 standard; DNA; 1647 BP.

XC AAS52489;

XX AAS52489;

XX DT 13-FEB-2002 (first entry)

XX Escherichia coli.

XX Antisense; ds; prokaryotic cellular

XW Antibacterial; drug design.

XX Antibacterial; drug design.

XX Antibacterial; drug design.

XX Antibacterial; drug design.

XX PM W0200170955-A2.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 21-MAR-2000; 2000US-0206848P.

XX 21-MAY-2000; 2000US-0205848P.

XX 21-MAY-2000; 2000US-027727P.

XX 21-MAY-2000; 2000US-0253625P.

XX 21-MAY-2000; 2000US-0253625P.

XX 21-MAY-2000; 2000US-0253625P.

XX 21-MAY-2000; 2000US-0259308P.

XX 21-MAY-2000; 2000US-0259308P.

XX (ELIT-) ELITRA PHARM INC.

XX WPI; 2001-611495/70.

XX WPI; 2001-611495/70.

DR WPI; 2001-611495/70.
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Best Local :
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                                                                                                                               New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. coli DNA for cellular proliferation protein #211.
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                                                     6126; 511pp; English
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76.9%;
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Pred. No. 2.1e+03;
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RESULT 18
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DT 19-JUN-2003 (first of the first 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic cuseful for the antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous antisense nucleic acid sequence encodes an essential prokaryotic cullular proliferation protein. Note: The sequence data for this patent of did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
                                                                                                                                            New antisense nucleic acids, useful for identifor homologous nucleic acids required for celisolate candidate molecules for rational drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2002; 2002WO-US009107.
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1533 GTACTGCAACTCG 1521
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Carr GJ,
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                                                                                                                                                  useful for identifying proteins or screening required for cellular proliferation to for rational drug discovery programs.
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Yamamoto R,
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Forsyth
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                                                                                                                                                                                                                                                                                                                                                        Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression

SEQ ID NO 20432; 1766pp; English.

of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid

polypeptide whose expression is i

(2) a host cell containing the vector; (3) an isolated

inhibited by the antisense

nucleic acid; encoding a

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RESULT 19
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a proliferation of the compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a proliferation of the compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation or the compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits are compound that inhibits are compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits are compound that inhib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          malate:quinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fermentative preparation of L-threonine; Enterobacteriaceae bacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding Escherichia coli malate:quinone oxidoreductase (mgo).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2003
21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK13893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1647 BP; 400 A; 402 C; 488 G; 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug discovery programs, or for s
required for proliferation in cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
                                                                            18-JUL-2000; 2000DE-01034833.
30-JAN-2001; 2001DE-01003874.
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200206459-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK13893 standard; DNA; 1720
(DEGS ) DEGUSSA AG
                                                                                                                                                                                                                            16-MAY-2001; 2001WO-EP005548
                                                                                                                                                                                                                                                                                                                       24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dentifying proteins or screening for homologous nucleic acids required or cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae or P. aeruginosa. The present sequence is one of the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTACTGCAACTCG 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli; strain MC4100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Mgo"
'EC_number= "1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.9%;
76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "1.1.99.16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13; DB 8;
Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mgo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fermentation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H
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XXXXXXXX
Permentative preparation of L-threonine by employing Enterobacteriaceae bacteria in which nucleotide sequence(s) that code(s) for malate:quinon
                                                                                                                                                           Rieping M,
                                                                                                       oxidoreductase (mgo)
                                                                                                                                     WPI; 2002-217000/27.
P-PSDB; AAU75255.
                                                                                                                                                            Thierbach
                                                                                                        gene
                                                                                                                                                            Ģ
                                                                                                        are
                                                                                                                                                            Van Der Rest
                                                                                                        enhanced,
                                                                                                                                                            ğ
                                                                                                        particularly
                                                                                                                                                            Molenaar
                                                                                                                                                            ū
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Claim 2; Page 30-32; 39pp; English over-expressed.

The present invention relates to a process for the fermentative preparation of L-threonine. The process involves employing preparation of L-threonine. The process involves employing Enterobacteriaceae bacteria, particularly those which already produce threonine, and in which the gene which encodes for the malate:quinone oxidoreductase (mgo) enzyme (E.C.1.1.99.16) are enhanced, in particular coxidoreductase (mgo) enzyme (E.C.1.1.99.16) are enhanced. oxidoreductase (mgo) enzyme (E.C.1.1.99.16) are enhanced, in particular over-expressed. The invention employs the Enterobacteriaceae, Escherichia coli as an example. The process is useful for preparing L-threonine by fermentation. The present sequence encodes for the E. coli mgo enzyme. (Updated on 29-AUG-2003 to standardise OS field) already produce L-

Sequence 1720 BP; 414 A; 421 C; 516 G; 369 T; 0 U; 0 Other;

밁 8 Best Local Matches 1 Query Match |:||:||||:|| 1482 GTACTGCAACTCG 1470 2 GUACUGCAACUCG 14 Similarity Conservative 92.9%; ω --Score 13; Pred. No. Mismatches 2.1e+03; DB 6; 0 Length 1720; Indels 0

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AAS92825/c
ID AAS928
XX
AC AAS928
                                                                       RESULT 20
                       AAS92825
                                               AAS92825 standard; cDNA; 1732 BP
13-FEB-2002
(first entry)
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DNA encoding novel human diagnostic protein #28629

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;

Homo sapiens

WO200175067-A2

X S X E X S X

11-OCT-2001

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

FXFXXFXFX FXFXXFXFX

Drmanac RT, Liu C, Tang ĭ

PXRRXRXRXRXRXRXRXRXRXRXR

P-PSDB; 2001-639362/73. DB; ABG28638.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation of presponsible for genetic disorders or other traits and to assess mutations

Claim 1; SEQ ID NO 28629; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain

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RESULT 21
AAS90081/c
ID AAS900
XX AAS900
XX AAS900
XX DNA en
XX Human;
XW Homo e
XX Homo
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 10
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1732 BP; 422
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                                                                                                                                                                                            Claim 1; SEQ ID NO 25885; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #25885.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-639362/73.
DB; ABG25894.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mapping; gene medical imaging;
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76.91;
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maging; diagnostic; genetic disorder; ss
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Pred. No. 2.1e+03;
3; Mismatches 0
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Best Local :
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26-MAY-2000; 2000US-0008408:
30-JUN-2000; 2000US-0008408:
03-AUG-2000; 2000US-00632366:
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359P.
04-OCT-2000; 2000GB-00024263:
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Pred. No. 2.1e+03;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a

gene expression

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4636; 487pp; English

genome-derived single exon nucleic acid probes useful for analyzing expression in human cervical epithelial cells.

Human

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RESULT 23
ABA56435
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023655P.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-00024263.
                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence dat for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful gene expression in human fetal liver.
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                                                        Sequence 1945 BP; 453 A; 617 C; 484 G; 391 T;
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The sequence data 
fication, but was
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GUACUGCAACUCG 14

ABA45908; 01-FEB-2002

(first entry)

Human; microarray; single exon probe; gene expression; breast; cancer; ss.

disease;

Human breast cell single exon nucleic acid probe #4603.

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ABA45908
ID AB*
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AAI36072
ID AAI36
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                                                                                                                                                                                                                                                                                                          WPI;
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  ABA45908 standard; DNA; 1945
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genetic disorder; ss.
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03-AUG-2000; 2000US-00632366.
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                                                           263 GTACTGCAACTCG 275
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GTACTGCAACTCG 275
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76.9%;
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RESULT 26
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XX Probe
XX Humar
KW Cardi
KW Conge
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                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived CC from human breast and BT 474 cells. The method involves contacting the CC probes with a collection of detectably labelled nucleic acids derived CC from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the CC expression of regions of genomic DNA predicted to encode proteins. They CC are useful for gene discovery, and for determining predisposition and/or CC prognosing breast disease. Gene expression analysis is useful for cc assessing the toxicity of chemical agents on cells. The microarray of CC this invention presents a far greater diversity of probes for measuring CC microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon cucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained con electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                 Matches
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
              Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                             Probe #4533
                                                                                                            23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                           Sequence 1945 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                            ABA26067;
                                                                                                                                                                       ABA26067 standard; DNA; 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4603; 327pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                     263
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2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-023469P.
; 2000US-0236359P.
; 2000US-0236359P.
                                                                             for gene
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                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                            453
                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                            92.9%;
76.9%;
                                                                           expression analysis in human heart cell sample
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Pred. No. 2.1e+03;
3; Mismatches 0
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                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                            484 G;
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Best Local Similarity
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840R.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 04-FEB-2000; 2000US-0180312P
26-MAY-2000; 2000US-0207456P
                                            30-JAN-2001; 2001WO-US000668
                                                                         09-AUG-2001
                                                                                                                                 Homo sapiens
                                                                                                                                                            microarray; cancer;
                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                  AAK30108;
                                                                                                                                                                                                                                                                                              AAK30108 standard; DNA; 1945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1945 BP; 453 A; 617 C; 484 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                                                                      WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                    263 GTACTGCAACTCG 275
                                                                                                                                                                                                          bone
                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon nucleic acid probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                 2 GUACUGCAACUCG 14
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                                                                                                                                                                                                       marrow expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000US-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                            leukaemia; lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
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                                                                                                                                                                                                                                                                                              ВP
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Pred. No. 2.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                         probe SEQ
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234359P.
04-OCT-2000; 2000GB-00024263.
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                       30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                         Human brain expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                      AAK04600;
                                                                                                                                                                                                                                                                                                                                                                                           AAK04600 standard; DNA; 1945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human bone marrow.
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                               WPI; 2001-483446/52
                                                                                                                                                                                                                                  WO200157275-A2
                                                                                                                                                                                                                                                                                         Alzheimer's
                                                                                                                                                                                                                                                                                                    Human; brain expressed
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                                                                          MOLECULAR DYNAMICS INC
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                                                     Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4665; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                        n expressed exon; gene expression analysis; probe; microarray; disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
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76.9%;
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Single exon nucleic brains.

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expression

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Best Local
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        The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                   Claim
                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human liver single exon probe,
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                                                                                                                                                                                            Human
                                                                                                                                                                                                                        WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                              (MOLE-)
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                                                                                                                                                                               expression in human
                                                                                                                                                                                                                                                  SG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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                                                                                                                                                                              genome-derived single exon nucleic acid probes useful expression in human adult liver.
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                                                                                                                                                   SEQ ID NO 4747; 658pp; English.
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; 2000US-0236359P.
; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                   2000US-00632366.
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                                                                                                                                                                                                                                                  봈
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76.9%;
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Pred. No.
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RESULT 30
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234587P.
27-SEP-2000; 2000US-0234359P.
04-OCT-2000; 2000GB-00024263.
                                                                        The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form at the printed specification, but was obtained in electronic format different with a part of the presence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from W
                                                                                                                                                                                                                                                                                      Novel single exon
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                                       Sequence 1945 BP;
                                                                                                                                                                                                                                                Claim
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DB 5; 1
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RESULT 31
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CC nucleic acid probes for measuring gene expression in a sample derived (from human lung comprising single exon nucleic acid probes having one of (22614 nucleic acid sequences mentioned in the specification, or their (22614) complements or the 1287 open reading frames derived from the 12814 (226) probes. Also included are a microarray comprising the novel set of probes (226) the novel set of probes which hybridise at high stringency to a nucleic (226) caid expressed in the human lung; measuring gene expression in a sample (226) caid expressed in the human lung; measuring gene expression in a sample (236) contaction of detectably labeled nucleic acids derived from human lung; comprising (a) contacting the array with a (236) contacting the array with a contacting the array with a contacting the bound to each probe of the (236) contacting the contacting the array with a conta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spatially-addressable set of single exon nucleic acid probes, used
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27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene expression in human lung samples
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RESULT 32
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New isolated protein complexes useful for diagnosing a disease or disorder, or as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (CODD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
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                                                                                                             P-PSDB; ABR53183
                                                                                                                                                                                            Bauer A, Ga
Marzioch M,
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Pred. No. 2.1e+03;
                                                                                                                                                                                                                         Krause R,
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The invention relates to multiprotein complexes from eukaryotes. Protein of the invention and DNA sequences encoding them are given in records ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are obtainable by using a protein as a bait and isolating the set of protein

proteins

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le by using a protein as attached thereto from co

Disclosure;

SEQ ID NO 1232; 17pp +

Sequence Listing; English.

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RESULT 33
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Marzioch M, Grandi r
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                                                  useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament
                                                                                                                                                                                                                                                                                                                                        The invention relates to novel protein complexes comprising a first second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defin the specification. The variants are encoded by nucleic acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins and protein complexes from eukaryotes, useful as targets drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or
                                                                                                                                                                                                                                                     hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
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)B; ADK63218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1470;
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i P, Krause R,
n C, Rick J;
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ruse U, M
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            CC The invention relates to isolated polymucleotide (I) and polypeptide (II) CC sequences; (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polymucleotides are also used CI in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal CC useful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The CC polypeptide and polymucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this catent did not appear in the printed specification, but was obtained in CC electronic format directly from MIPO at the content of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 23995; 103pp; English.
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ARTSULT 35
ART93 ART93
ARC PSD-9
KW PSD-9
KW PSD-9
KW Duche
KW Duche
KW Barcc
KW WP1;
DR WP1;
DR WP1;
DR WP1;
DR P-PSI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSD-93; nNOS; neuronal nitric oxide synthase; Alzheimer's disease; diagnosis; muscular dystrophy; skeletal muscle; Huntington's disease; Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin; sarcolemma; PDZ domain; neurodegenerative disease; gene therapy; amyotropic lateral sclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2133 BP; 518 A; 542
                                                    Claim 17;
                                                                                                                 Diagnosing muscular dystrophy by detecting absence or decrease of neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma using new nNOS binding post-synaptic density proteins, PSD-93 and PSD-95; also used for the diagnosis, prophylaxis and treatment of stroke and
                                                                                                                                                                                                                                            WPI; 1997-470555/43.
P-PSDB; AAW34659, AAW34660, AAW34661, AAW34662,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-1996;
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                                                                                                                                                                                                                                                                                                                        DS,
                                                                                                  neurodegenerative diseases.
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10; Conserv
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                                               Page 72-73; 124pp; English
                                                                                                                                                                                                                                                                                                                     Brenman JE,
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/note= "PSD-93 page 12845. .2961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      '*tag= e
/note= "PSD-93 partial sequence (see AAW34663),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "PSD-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "PSD-93 partial sequence (see AAW34659)"
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 Mismatches

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Pred. No.
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                                                                                                                                                                                                                                                                                                                        DS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            # (pos: 2137. .213 partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  partial
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                                                                                                                                                                                                                                                 AAW34663
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This sequence encodes the post synaptic density protein-93 (PSD-93).

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RESULT 36
AAS90082/c
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 can be used in the method of the invention, for diagnosing muscular dystrophy (MD) in a mammal by detecting absence a decrease of neuron nitric oxide synthase (nNOS) in a skeletal muscle sample. Patients with Duchenne or Becker MD lack normal levels of nNOS in skeletal muscle, in addition to lack of functional dystrophin, nNOS is normally targeted to
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS90082 standard; cDNA; 3222
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                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                   Liu C,
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Pred. No. 2.2e+03;
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밁 8

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain

The present invention relates to Aspergillus fumigatus genes that are essential and are potential targets for drug screening. The methods and compositions of the present invention are useful for diagnosing and/or treating invasive Aspergillus fumigatus infection, including the allergic forms of the disease, such as Farmer's lung disease. They can also be

New purified or isolated Aspergillus fumigatus nucleic acid molecule encoding a gene product, useful for diagnosing and/or treating invasifungal infections, such as Farmer's lung disease.

and/or treating invasive

Claim 3; SEQ ID NO 543; 164pp; English.

SEQ ID NO 25886; 103pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal? CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular waist markers and as a food CC polypeptide in tissue, as molecular are useful in medical imaging CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC coding sequences. AAS64197-AAS94564 represent novel human diagnostic CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local (
                                                                                                                                                                          WPI; 2004-594200/57.
                                                                                                                                                                                                   Jiang B,
                                                                                                                                                                                                                               (BLIT-)
                                                                                                                                                                                                                                                                       17-JAN-2003; 2003US-0441281P
13-JUN-2003; 2003US-0478196P
                                                                                                                                                                                                                                                                                                                16-JAN-2004; 2004WO-US001099
                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                              Fungicide; Aspergillus fumigatus infection;
drug screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aspergillus fumigatus essential gene genomic sequence #543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADR84732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR84732 standard; DNA; 3443 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3222 BP; 727 A; 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                               P-PSDB;
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                                                                                                                                                                                                                               ELITRA CANADA LTD.
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                                                                                                                                                                                                    .Hu W, Lemieux S,
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                                                                                                                                                                                                      Roemer T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Farmer's lung disease;
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RRESULT 38
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                                                                                                                                                                                                                                                                                                       AAX20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnost characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis.
                                                                                                                                                                                                                            Sequence 14063 BP; 3225 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX20500 standard; DNA; 14063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 178-186; 1150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence from the genome of Treponema pallidum.
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CGTACTGCAACTC 5707
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                                                                                                               Conservative
                                                                                                                                                                                                                                                                                     products such as enzymes
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76.9%;
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76.9%;
                                                                                                                                                                                                                            4086 C;
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Pred. No.
                                                                                                                                    Score 13; DB 2;
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     syphilis; Borrelia infection; animal;
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                                                                                                               Mismatches
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2.2e+03;
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                                                                                                                                                                  Length 14063;
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RESULT 40
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RESULT 39
ADZ13310/c
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                                                                                                                                                                       with a composition comprising the polypeptide or its antigen binding care fragment and collecting cells from the host expressing antibodies against the antigen antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of dagnosing cancer, a composition comprising cancer and a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents murine cancer—associated genomic DNA of the invention.
                                              Matches
                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated (CA) nucleic acid, comprising two or more nucleic acid proben the invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal binds to a polypeptide, which is prepared by immunizing a host animal
                                                                                                                         Sequence 83493 BP; 22528 A; 17868 C; 19019 G; 24033 T; 0 U; 45 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid array useful for detecting cancer comprises two or more nucleic acid probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 830; 198pp; English
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                                                                                                                                                               invention.
                                            l Similarity
10; Conserv
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CGUACUGCAACUC 13
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                                              Conservative
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Pred. No.
                                                Mismatches
                                                                DB 14;
2.6e+03;
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RESULT 42
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ARB39175 12/c
Continuation (13 of 35) c
WP Sequence split into 3:
WP Pragment Name
WP ARB39175 00
WP ARB39175 00
WP ARB39175 02
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Continuation
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32 CGTACTGCAACTC 34744
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2.6e+03;
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Accession Aeb39175
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New genome of Legionella pneumophila Paris strain and polypeptides, useful for detection or identification for treatment and prevention of infections.
                                                                                                         Claim 1; SEQ ID NO 54; 660pp; English.
                                                                                                                                      and
                                                                                                                               nd derived
                                                                                                                                strain
                                                                                                                                and
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The invention relates to an isolated or purified nucleotide sequences (I) from Legionella pneumophila Paris strain. (I), and their related sequences or fragments are useful as primers and probes for detection and amplification, including differentiation between the Paris and Philadelphia strains of Legionella pneumophila and to prepare recombinant (hybrid) polypeptides (II) (II) are also useful for preparation of specific antibodies (Ab), also used for detection/identification of Legionella, and some (I), specifically those involved in synthesis of surface proteins, are targets for identification of inhibitors. (II), or vectors that contain (I), are useful as vaccines and immunogenic compositions, for treatment and prevention of infections by L. pneumophila. The present squence represents a L. pneumophila DNA.

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Sequence 184368 BP; 57341 A;
33604 C; 36303 G;
  57120 T; 0 U; 0 Other;
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Ś Query Match
Best Local Similarity
Matches 10; Conserv CGUACUGCAACUC 13 Conservative 92.9**%**; 76.9**%**; <u>ب</u> Score 13; Pred. No. Mismatches DB 14; Le. . 2.7e+03; 0; Length 184368; Indels 0; Gaps 0

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119323

CGTACTGCAACTC 119311

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08-SEP-2005
                                   AEB39170
                                  standard; DNA;
(first
entry)
                                   207461
                                   BP
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detection; infection; Antibacterial; Vaccine; pneumophila DNA SEQ ID NO 3502. d**e**;

WO2005049642-A2

Legionella pneumophila.

02-JUN-2005

23-SEP-2004; 2004WO-IB003578

21-NOV-2003; 2003FR-00013687.

(INSP) INST PASTEUR.
(INRM) INSERM INST NAT SANTE & RECH MEDICALE
(IYLY-) UNIV LYON I BERNARD CLAUDE.
(CNRS) CNRS CENT NAT RECH SCI.

Buchrieser (Rusniok C, Jarraud S; C, Tichit M, Bouchier C, Zidane Btienne J, Ma L, Magnier Magnier ۶ Cazalet C, \, Kunst F, Glaser P; Vandenesch

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WPI; 2005-388305/40.

New genome of Legionella pneumophila Paris strain and polypeptides, useful for detection or identification of treatment and prevention of infections. derived of the strain

Example 9; SEQ ID NO 3502; 660pp; English

The invention relates to an isolated or purified nucleotide sequences from Legionella pneumophila Paris strain. (I), and their related sequences or fragments, are useful as primers and probes for detection sequences primers Ê

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compositions, for treatment and prevented a L. pneumophila DNA.
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                                                                                                                                                                                         nucleotides where one of the nucleotides is polymorphism (SNP), useful for diagnosing or
                                                                                                                                                                                                                                               WPI; 2004-728480/71
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25-APR-2003; 2003US-0465241P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systemic lupus erythematosus; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single nucleotide polymorphism detection; SNP detection;
rheumatoid arthritis; type 1 diabetes; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human autoimmune disease-related SNP context sequence -
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The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for disgnosing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory beautiful actions and protein account of the invention of the contact of the invention are useful for disposing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1

pernicious

Claim 16; SEQ ID

NO 2475; 123pp; English

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                                       The invention comprises amino acid and coding sequences containing genetic polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA and protein sequences of the invention are useful for disgnosing and treating autoimmune disease, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory bowel disease, psoriasis, throiditis, celiac disease, permicious anaemia, asthma, vitiligo, glomerulonephritis, Grave's disease, myocarditis, Sjogren's disease, or primary systemic vasculitis. The myocarditis, Sjogren's disease, or primary systemic vasculitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; celiac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
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                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule comprises at least 8 contiguous nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune diseases, e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-2003; 2003US-0455444P.
25-APR-2003; 2003US-0465241P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human autoimmune
             present DNA sequence represents a human autoimmune disease-related genomic-based SNP context sequence of the invention. NOTE: The pre
                                                                                                                                                                                                                                                           Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                        Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                        (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-2004; 2004WO-US008461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primary systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; type 1 diabetes; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single nucleotide polymorphism detection; SNP detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGUACUGCAACUC
                                                                                                                                                                                                                                                         SEQ ID NO 5835; 123pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        Begovich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease-related SNP context sequence -
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76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                        ΑΒ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                         Alexander HC;
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Pred. No. 3.
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RESULT 49
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                         used to clone a fragment of the human OGFr cDNA. The complete sequence of human OGFr was assembled with a combination of 3' and 5' RACE. 5' RACE consistently yielded a single species of cDNA, while the 3' RACE revealed extensive alternative splicing. The alternate splice forms were missing the imperfect repeats or differed in the number of imperfect repeats. The human OGFr gene chromosomal location was determined by FISH as 20(13). expression vector are useful for detecting expression or levels of an OGFr in a tissue. OGFr nucleic acids can be used to inhibit growth of cells in vitro. The antisense sequences and antibodies can be used to promote growth of cells in vitro. Cell growth can be promoted by interfering with the OGF ligand-receptor system, especially where a subject suffers from a tissue wound. Treating cancer comprises enhancing the function of the OGF ligand-receptor system in cancerous cells of a patient or administering the OGFr nucleic acid to the patient
                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primers generated from rat opioid growth factor receptor (OGFr) cDNA were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 77-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cDNA encoding rat modulate cell growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1998;
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                                                                                                                   470 A;
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                      4.
                                          Score 12.6; DB 3;
Pred. No. 3.6e+03;
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                                                                                                                   G; 297
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CGUACUGCAACUC 13 ||:||:||||:| CGYACTGCAACTC 14186 Query Match Best Local S Matches 10

Similarity

90.0%;

Score 12.6; DB 13 Pred. No. 4.2e+03;

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                         The invention comprises amino acid and coding sequences containing comprises polymorphisms associated with an altered risk of developing an autoimmune disease (e.g. rheumatoid arthritis). The invention further comprises a method of identifying an individual that has an altered risk of developing an autoimmune disease, comprising detecting a single nucleotide polymorphism (SNP) in a nucleic acid of the invention. The DNA compressing and protein sequences of the invention are useful for diagnosing and treating autoimmune diseases, such as: rheumatoid arthritis, type 1 diabetes, multiple sclerosis, systemic lupus erythematosus, inflammatory compositions as the protein sequence of the inventions of the invention of the invention of the invention of the present sequence is not genomic DNA sequence of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single nucleotide polymorphism detection; SNP detection; rheumatoid arthritis; type 1 diabetes; multiple sclerosis; systemic lupus erythematosus; inflammatory bowel disease; psoriasis; thyroiditis; ceilac disease; pernicious anaemia; asthma; vitiligo; glomerulonephritis; Grave's disease; myocarditis; Sjogren's disease;
Sequence 29871 BP;
                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid molecule comprises at least 8 contiguon nucleotides where one of the nucleotides is a single nucleotide polymorphism (SNP), useful for diagnosing or treating autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cargill M,
                                                                                                                                                                                                                                                                                                 Claim 16;
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25-APR-2003; 2003US-0465241P.
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8723 A;
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Submitted (01-JUL-1996) O. Faktor, The Hebrew University of Submitted, Department of Encomology, The Faculty of Agriculture, P.O.Box 12, Rehovot 76100, ISRAEL Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            large subunit; ribonucleotide reductase. Spodoptera littoralis nucleopolyhedrovirus Spodoptera littoralis nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Bacul
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/isoTate="E15"
/specific host="Spodoptera littoralis"
/db xref="taxon:10456"
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AC093956 Oryza sat
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AP914084 Triticum
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BX784032 Zebrafish
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                                              JOURNAL
REFERENCE
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AUTHORS
TITLE
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ORGANISM
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VERSION
KEYWORDS
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AF484941/c
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Matches 11
AUTHORS
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Local Similarity
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Fusarium
                                                                                                                                                                     1 (bases I to 10151), Madrid, M.P., Di Pietro, A. and Roncero, M.I.G.
Madrid, M.P., Di Pietro, A. and Roncero, M.I.G.
Class V chitrin synthase determines pathogenesis in the vascular wilt fungus Fusarium oxysporum by mediating resistance to plant
                                                                                                                                                                                                                                                                              Fusarium oxysporum
Fusarium oxysporum
Rukaryota; Pungi; Ascomycota; Pezizomycotina; Bordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusari
Fusarium oxysporum complex.
2 (bases 1 to 10151)
2 Madrid, M.P., Di Pietro, A. and Roncero, M.I.G. Direct Submission
Submitted (18-FEB-2002) Departamento de Gene
                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF484941
AF484941.1
                                                                                                                                                                                                                                                                                                                                                                                                Fusarium oxysporum
                                                                                                                                              defense compounds
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/db_xref="Ini Proc\Trenel:041269"
/db_xref="Ini Proc\Trenel:041269"
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/db_xref="Ini Proc\Trenel:041269"
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GIYPGVTTVELDLLILAETAABRTIDHSDYSLLINAENGYPTHAB FTLFSAATPKAQMSSCF
AIDQKTGAATPMISDETYGLIGCAMISKSGGGIGFFYHNVRAKGSSVAGVDGAANGLVPMLR
ITVERPQYMMRVAIGHGRAFAVYVEPWHADVEDFLDLKGTGKTGKEEVRARELFYALMIP
VYNNTARYVNQGGNKRPGAFAVYVEPWHADVEDFLDLKGTGKVEKVARQATLWRAI
VYNNTARYVNQGGNKRPGAFAVYVEPWHADVEDFLDLKGTGKVEKVARQATLWRAI
ILAQVETGFTPYMLYKDSCNKKSHQSNLGTIKGSNLCTEIVEYTSKOEVAAVCNLASIAV
NKFVAPQPGVYDFERLKEITKSCDRNLNRIIDANQCFLREAERSNQRNRPIGIGVQGM
ADAFVTWRMFPESDAAAELNKKIFTITYGALEANCELAAKGGFYETYKOSPASROGL
QYDMNNGATPSNLMPMSLLKSKISKYGLRUSLLLAFMUTASTAQILGNNESFEPTTSN
IYQRRVLSGBFQVVNRHLVKDLAAIGLMNDTMKNLIMYNNGSVQNIESIPFBIRQLYK
TYMENSMRTMIRMAADRGAFIDQSQSFNVYNAEPSYGGLESILFYAMKNGLKTGMYYL
TYTENSMRTMIRMAADRGAFIDQSQSFNVYNAEPSYGGLESI
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2737. .2740
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/codon_start=1
/proteIn_id="CAA67424.1"
/proteIn_id="CAA67424.1"
/db_xref="01:2244678"
/db_xref="UniProt/TrEMBL:041270"
/translation="MSVSVNSPTLQDLLDAQKYA"
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/protein_id="CAA67423.1"
/db_xref="G1:2244677"
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/note="putative"
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/codon_start=1
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Pred. No. 5.9e+03;
3; Mismatches 0;
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Xanthomonas axonopodis pv. citri
Xanthomonas axonopodis pv. citri
Bacteria; Proteobacteria; Gammapı
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                                                                                                                                                                         the complete genome. AE012045 AE008923
                                                                                                                                                                                                                                               Xanthomonas axonopodis
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VSKEIVEDYSTIRVTLHMKNLLHLIGEDRYLTTLLLKYHSKYKTKYLESAQAWTIAPD
SWSVELSQRRRWINSTUHLABLIFLAGLGGFCCESMEFVVEIDLLSTIVQPVIVMY
VYLIYQVATNPSVVPITAFLLLGAIYGLQAVIFILRKMEMVGMMIMYIAAIPVESFG
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MGKI YSGLYEVQGH I VPPMV I VKVGKPSEVSRPGNRGKRDSQMVLMRFLNRVHYNLAM
SPMELEMYHQ I RNI I GVNPTFYEYLFQ I DADTVVAADSATRMI SAP I DDTRLI ACCGE
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WREKVAINMLIWLMCAVAAFFMVGFFMLICPKQYVYSSNELSSYDGDKGSKGAYVAIR
GFVIDLNAF1PNHYPGSNLVSEDTLLMYARQGYHALFSPSKCLPLCQGKUGQIPPEVT
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AQAKLPGSNFMTENTSAVFTVKHFAGEVDYPVKGLIEENGEIISGDLLNMINGTKSEF
VARLFGQDALQTVTHPNERTTVMQATVSSKPMRAPSVMSRKTHRTGRPSTAYKRQQQB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTARDDVRSEISGYSYATKAQGPFSBYGGGYQPSRPGSTAGFGHQNMSRMSLAHSEMF
GNRASQFGGSQFFSPEDLVGMPSDDALLABIRDILKTADLMTVTKKGIKQELBRRFNV
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ASILHIGQLEFETTSQTSVTGDDSGGFSHEGGTTITAVKNKDVLSIIAAFLGVSAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAISVMLASILVFKFLAALQFGGKNVPENLDKFVMCMIPAYTEDEDSLRRAIDSLSRM
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YSPKYVKKLARDSSWNVVT I HGKVYDMTKYLQGGLRLKAKAGKPTPN I PGATDFMEDS
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LGESGAGKSTIRAHLLTALLNKSSTPLSTKLSLAAYVFDSLTTTKTATTPTASKSGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPLYSFWHMDDFNWGNTRVIAGEAGKKIAVSDEGKFDPNSIPRKKWEEYQAELWETQT
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/protein_id="AAO49384.1"
/db_xref="GI:28628849"
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                                                                                                                                            GI:21110361
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78.6%; E
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Pred. No. 5.2e
3; Mismatches
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3 pv. citri
. citri str. 306
. citri str. 306
Gammaproteobacteria; Xanthomonadales;
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5.2e+03;
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Miyaki,C.Y., Moon,D.H., Moreira,L.M., Novo,M.T.M., Okura,V.K.,
Oliveira,W.C., Oliveira,V.R., Pereira,H.A. Jr., Rossi,A.,
Sena,J.A.D., Silva,C., de Souza,R.F., Spinola,L.A.F., Takita,M.A.
Tamura,R.B., Teikeira,B.C., Tezza,R.I.D., Trindade dos Santos,M.,
Truffi,D., Tsai,S.M., White,Fr., Setubal,J.C. and Kitajima,J.P.
Comparison of the genomes of two Xanthomonas pathogens with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonadaceae; Xanthomonas.
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Truffi,D., Tsai,S.M., White,F.F., Setubal,J.C. and Kitajima,J.P.
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                                                                                                                                                                                                                                                                                                                         ATRHLTEAIGYRKLDRALGAASAA'
                                                                                                                                                                                                                                                                                                                                                           IRRYRSRISGPLLDRIDLHVEVPRLPPQALRSGNLGEDSASVRARVVAARQRQLARGA
LPNAQLDQADTDRHCRLQHNDQVLLERAIEQLQLSARSMHRILRVARTIADLDDSADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="comM"
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                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MDRSAAQNFLTPVGDLRIVHYVAYVCTSGWAGDGSGRCRCSSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specificities
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Leite, R.P. Jr., Lemos, B.G.M.
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748, Sao Paulo,
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.A., Almeida, N.F.
Camargo, L.B.A.,
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SP 05508-900,
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YNTGSLPRQPGQVMMRIVRHAFPSRPKPVRQGSGALQSA"
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                                                                                                                                                                                                                                                                                                                                         complement (5298. .6374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSATSAVTAHIIEMAKTLRLRTIAEGVERQEQLDYLRAHGVDLAQGWLFSRALPATGF
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RSLMDIDAARTTITHLRGAGHTVSIDDFGTGYSSLQYLQGLPLDALKIDKSFVDTIGT
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located using Blastx/Glimmer/Genemark"
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                                                                                                                                                                       product="oxidoreductase"
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                                                                                                                                                                                                                                                                                    putative; ORF
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ORGANISM
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     JOURNAL
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                       aerophilum
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Pyrobaculum aerophilum str. IM2
Pyrobaculum aerophilum str. IM2
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                 complete genome.
AE009858 AE009441
AE009858.1 GI:18160615
                                                                                                                                                                                                                                                                           AE009858
Pyrobaculum aerophilum strain
                                                                                             Thermoproteaceae; Pyrobaculum.
1 (bases 1 to 14169)
                                     Genome sequence of the hyperthermophilic crenarchaeon
                                                                            Fitz-Gibbon, S.T., Ladner, H., Kim, U.J.,
                                                                                                                                                                                                                                                                                                                                                                                                 CGTACTGCAACTCG 9479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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QVQLSRSGRTLTLPRCQSLLEGLEAQGLRPKHGCRMGICNTCACPRQSGTTRHLLTGE
RSNEPTAQVRLCISAPSTDLILDL*
6467. .7114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="XAC3964"
8775. .9899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTSIALPSHDAPPSRKPAISREDLIAAALSLIGPHRSLSTLSLR
EVAREAGIAPNSFYRQFRDMDELAVALIDLAGRSLRTIIGQARQRATSTDRSVIRVSV
EAFMEQLRADDKLLHYLLREGAVGSDAFKQAVERELTYFEDELRVDLIRLAAADNAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSDLASPGDMRARSTRDEVSSRLPSAHRPLCEAKLARSTDARRL
AQCSACGTSAKHLTAPFSPSDGSIAGDGFRSLRKPRGSTQHERVQCVAWAWVTRHTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="XAC3962"
7240. .7560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identified by sequence similarity; putative;
located using Blastx/Glimmer/Genemark"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identified by sequence similarity;
located using Blastx/Glimmer/Genemark"
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/gene="XAC3964"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
/protein_id="AAM38799.1"
/db_xref="GI 21110369"
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/transl_table=11
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/transT_table=11
/product="transcriptional regulator tetR family"
/protein_id="AAM38798.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Found by tRNAscan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="tRNA-Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="GI:21110368"
  Acad.
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Sci. U.S.A. 99
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Pred. No. 5.1e+03;
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                                                                            Stetter, K.O., Simon, M.I. and
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113 of 201
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the
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University of California, Los Angeles, 405 Hilgard Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Fitz-Gibbon, S.T., Lad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Angeles,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11792869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2706. .3257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKPAFPVNVSVNEVAAHYTAKRGDSLKIPKTGLVKIDVGAQRDGYIVDAAVTVTIGPV
FNNLQKAAKSALESAINAAKPGIKAWQIGEVVERVIKSFGLSPIYNLTGHKVERYLLH
AGHVIPNYSDKTASQALAPGDVYAIEPFATNGEGYVVDGGEITIYRLARWRHKNYQHL
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                                                                                                                                                                                                                                  KDIIAIGVILLIVILLFRKRSWV"
                                                                                                                                                                                                                                                        /trānblation="mlabyvaqrvaliqerayhrlvvilsatsmssvmmsglalffeb
afkylslallalgvllsrrvlrnabekirkfmanverbamarryfatlkbyynfidyl
tklyabptibdfilaabkkkirastylfsqsttalraknrlvititaltisiphlvln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NALKVAVEAASMILRIDEIIAASKLEKEKEEKKEEKKEEFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERNLDDALSVVSDVVEDPYILPAGGAAEIEAAKAVRAFAPKVGGREQYAVEAFARALE
VIPKALAENAGLDPIDILTELTHKHEQTDGWKYGLDVYQGKVVDMVSLGLVEPLTVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARLVTSIEDLTEADLGFAGLVEERRVGDEKMVFVEQCKNPKAVSILVRGGFERLVDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>QLVYGIVVDKEVVHAAMPKRVVNAKIALLDAPLEVEKPBIDABIRINDPTQMRAFLEB</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIAMTSMGGKISETVKEYFADLAVKAVLQVAEERNGKWYVDLDNIQIVKKHGGSLLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mSQAVLTQIGGVPVLVLKEGTQRAFGKEALRLNIMIARAIAEVM
RTTLGPKGMDKMLIDSLGDITITNDGATILDEMDVQHPIAKLLVBISKSQEEEAGDGT
TTAVVLAGALLEBAEKLLEKNIHPTVIVSGFKKALDVAAEHLRKVAIPVNRTDVDTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pyrobaculum aerophilum str. IM2"
/mol_type="genomic DNA"
/strain="IM2"
                                                                                                                                           complement (3247. .4278)
                                                                                                                                                                              /gene="PAE2119"
                                                                                                                                                                                                     complement (3247. .4278)
                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="AAL63958.1"
/db_xref="GI:18160618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="PAE2118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="AAL63957.
db_xref="GI:18160617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PAE2117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :DIISAEAGPLPFTPRWFPQLTDDAIREALKAGVLQGYEVLVERSKGFVAQFEDTVYV
product="conjugal transfer protein, conjectural"
protein_id="AAL63959.1"
                                                                                                                                 'gene="PAE2119"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1
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db_xref="GI:18160616"
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                                                       transl
                                                                                                      note="Unclassified"
                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="PAE2118"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="PAE2116"
                                                                                                                                                                                                                                                                                                                                                                                                                 transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ranslation="MLRILRQVGDVVNKALKYALDLTQPDMPVLELCERVEAFIRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _xref="taxon:178306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lement (2706. .3257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (chaperonin) alpha subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stabilization"
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gene CDS

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gene CDS

/gene="PAE2127" complement (6700.

.7077)

'gene="PAB2127"

product="paREP2a"

table=11

note="Hypothetical; Conserved within genome"

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trānslation="MKCPYCQSMNITLADGEYVCRDCGTVLGPEVVPPRPRQVLPVPV/trānslation="MKCPYCQSMNITLADGEYVAEALGVPEVTVVALQIFQRLDKRIYQ
RHKLIMLALEQENKKSIKKKYSEMVKMYTGKVAEALGVPEVTVVALQIFQRLDKRIYQ
GKSPRVIAAAVAYLAAERLGIYIHKQVIAKILGVSKPSIRDTASRLRKYVPNIKETT"
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SIDETLDRRYGVLERINEKWAIRGYLATVGLEELSPFLEDREVEDIVVIPGRPIYITR
KSGKEKADVTAELKTVKSLLKIAYLKGVELTTSNPSLRYGLKLGDLRLRISLDLPPVV
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                                                                                                                                                                                                                                                                                                                                                                                                          complement (5871. .6710)
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                                                         WEGEWRGKSMSCFVTEKRAVCKVGEKMAAPYVFDTPHGVYLRPEIKLVDDWIKVAHRG
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                                                                                                                                                                                                                                                                                                                                                   note="Hypothetical; Conserved within genome"
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Direct Submission
Submitted (09-JUL-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(B-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA, clone;OJ1111_B02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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96360 bp DNA linear Oryza sativa (japonica cultivar-group) chromosome 8
0J1111_B02, *** SEQUENCING IN PROGRESS ***.
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Sasaki, T., Matsumoto, T. and Yamamoto, K.
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VRAHWFIMAAAAAGGLAWAVVAQOLDTTLWGNHIALNAGAIAGLAKAAGYGKWTEKAVAGAYAVAAVATKTASEKEIVERAAQLGILDKGVVEKAVSAFSTLRHAMDEKQIENAVLELRRLTSY
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AL592045
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                          AL Submitted (13.MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 19, 2002 this sequence version replaced gi:25045216.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel:81-298-38-7441, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be replaced

* the accession number will be preserved.
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                                                 Center: Wellcome Trust Sanger Institute
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG;
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                                                                                                                                                                                           of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ellington, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                          Web site: http://www.sanger.ac.uk
                                                                                                                                       VECTOR: pBACe3.6
                                                                                                                                                                                                                         RP11-275I14 is from the library RPCI-11.1 constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Contact: vega@sanger.ac.uk
                                                                                                                                                                 http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 99251)
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/mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .96360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="0J1111_B02"
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                                                                                                               Genome Center
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; Pred. No. 4e+0:
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4e+03;
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                                                                                                                                                   polyA_site
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                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   except on the rare occasion of the clone being a YAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30); an attempt was made to resolve all sequencing problems, as compressions and repeats; all regions were covered by at one subclone; and the assembly was confirmed by restriction one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus tag="RP11-275114.1-001"
complement(join(16846. .18988,24502. .24786,26814. .2700
31351. .31525,33698. .33856,36956. .37096,38026. .38167,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Sequence confirmed by (AC044825 and AC021883)
sequenced by WIBR and WUGSC."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Sequence from AC044825 and AC021883 sequenced
WIBR and WUGSC."
                            /locus_tag="RP11-275I14.1-001" complement(join(18777. .18988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequenced
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/note="Single clone region.
complement (join (18777. .18988,24502. .24786,26814. .31551. .31525. 33698. .33856,36956. .37096,38026. .3
                                                                                        complement (16860. .16865)
                                                                                                                                                                        Em: BC039575
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restriction_digest data."
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                   gene="ACBD3"
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                                                                                                              tag="RP11-275I14.1-001"
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$1525,33698. .33856,36956. .37096,38026. .38167,
                                                                                                                                                                        Em: AB043587.2
Em: BC045533.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -Coenzyme
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d from a single pUC
                                                                                                                                                                           Em: AK025520.1
Em: BC060792.1"
                                                                                                                                                                                                                                                                                                                   Em: BI325049
Em: BM975030
                                                                                                                                                                                                                                                                                                                                                                                Em:BF341078
Em:BF875919
                                                                                                                                                                                                                                                                                                                                                                                                                         Em: AW452221
Em: BE048884
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                                                                                                                                                                                                                                                                                                                 Em:BG283448.1
Em:BG705952.1
Em:BI438303.1
Em:BM979013.1
                                                                                                                                                                                            Em: AY150218.1
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                                                                                                                                                                                                                                                                                                                                                                                                                         Em: AW601227.1
Em: BE673355.1
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                                                                                                                                                                                                                                                                                                                                                                                                       Em:BF510719.
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        4. .27000,
.38167,
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/note="Sequence confirmed by (AC044825 sequenced by WIBR and WUGSC." complement (61040. .61388) /locus tag="RP11-275114.2-001" /pseudo
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SVITVGRGEVVTVRVPTHEEGSYLFWEFATDNYDIGFGVVFEWTDSPNTAVSVHIVSES
SDDDEEEEENIGCEEKAKKNANKPLLDEIVFVYRRDCHEEVVAGSHQVPGRGVVLLKF
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berlrrebeberriebeerlrleookooimaalnsotavofooyaaooyfonyeoooil
                                                                                                                                                                        /note="Sequence confirmed by (AC044825
sequenced by WIBR and WUGSC."
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                                                                                                                                                                                                                                                                                                                                       /note="Sequence from uni-directional dGTP big dye-
terminator reads only."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Sequence confirmed by (AC044825 and AC021883)
sequenced by WIBR and WUGSC."
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pgsgrgpgasgeqpepgeaaaggaaeearrleqrwgpgleelyglalrffkekdgkap
                                                                                                                                                                                                                                                        note="Single clone region. restriction digest data."
                                                                                                                                                                                                                                                           restriction
                                                                                                                                                                                                                                                                                                                                                                                                                          Restriction digest data confirm
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Single clone region. Sequence generated from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44107. .44146
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translation="MLVNGHYQEFKTRFGIMTSGQTHMQNLPFGPFSRASSAASGSSS
SELSVCVLACPLTDIILLGTVAFTFDDVGKEDPATTTSCCFCNAAYKPRESEDTLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="novel protein"
protein_id="CAH71921.1"
db_xref="GI:55665956"
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/locus_tag="RP11-275114.4-001"
/standard_name="OTTHUMP00000038761"
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|Tocus tag="RP11-27511.4-001"
|product="movel protein"
|note="match: ESTs: Em:AI682391.1 Em:AW511419.1
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/standard_name="OTTHUMP00000035668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="acyl-Coenzyme A binding
'note="match: ESTs: Em:BE765013.1"
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db_xref="GI:55665957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Sequence from AC044825 and AC021883 sequenced by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocus_tag="RP11-275I14.1-002"
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7170. .20235.26770.
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AL Submitted (09-JUL-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: Basaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-28-38-7441, Fax:81-298-38-7468)
Tel:81-28-38-7441, Fax:81-298-38-7468)
On Aug 12, 2002 this sequence version replaced gi:14646817.
Genes were predicted from the integrated results of the following: (http://ccr.081.mit.edu/GENSCAN.html), FGENESH (http://www.softberry.com/), GeneMark.hmm (http://www.softberry.com/), GeneMark.hmm (http://pap.dna.affrc.go.jp/RiceHmM/), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHmM/), SplicePredictor (http://rgp.dna.affrc.go.jp/RiceHmM/), SplicePredictor (http://bioinformatics.iastate.edu/Ggi-bin/sp.cgi), sim4 (http://sp.dna.affrc.go.jp/RiceHmM/), BLASTW and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTW. ESTS represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is significant homology to any protein but with full-length cDNA or between the protein and 'like protein'. A gene without significant homology to any protein but with full-length cDNA or
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2 (bases 1 to 101249)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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BAC clone:OJ1136_A10.
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/note="Single clone region. Sequence generated from a short insert library derived from a single pUC clone. Restriction digest data confirm the assembly." 68859. .68868
/note="Single clone region. Assembly confirmed by restriction digest data."
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/locus tag="RP11-275114.2-001"
/locus tag="RP11-275114.2-001"
/note="match: proteins: Sw:P49207 Sw:Q29223 Sw:Q90YT5
/sw:Q9blr9 Tr:AAH58118 Tr:AAL87001 Tr:Q7SZ79 Tr:Q7ZWJ7"
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The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of OJI136 A10 clone has an overlap with P0703C03 (DDBU; AP004673) clone at 5' end and with P0670808 (DDBJ; AP004759) at 3' end. The sequence was generated by combining Monsanco and RGP-Japan sequencing data. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dua.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
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complement (4254. .6577)

/gene="0J1136 A10.101"

complement (joIn(<4254. .4478,5437. .5573,6496. .>6577))

/gene="0J1136 A10.101"

/note="start and end point are not identified"

complement (join(4254. .4478,5437. .5573,6496. .6577))

/gene="0J1136 A10.101"
                                                                                                   complement (21188. .23972)

// gene="CJ1156 A10.104"

// gene="CJ1156 A10.104"

// gene="CJ1156 A10.104"

// note="supported by full-length cDNA(s): AK120478"

complement (join(21565. .22363,22784. .23250))

// gene="CJ1156 A10.104"

// note="CJ1156 A10.104"
                                                                                                                                                                                                                                                                                                                                                                                            /translation="MMRLRRGHITQLLLLILAPVRLLQBITIBBAATTLAPPPPQTIS
SMIGSLRGRGRRLLAAASALALLLLLLSRSPRRRPHGYGVVLIDAGSTRSRVHVIAYR
SPAASAAAALPMIDMARTASMKAAPGCCPSPIRAAMVGRWRCSWSSLMVGGGBARH
GRVRQGGKSRGRVRLMVGGGBGRHGRVRRGGKSRGKRVRAAMLVWRAABIILFGV
RSFFRSFWRAVSFSGARRSVNPVLIATAGLIRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="OJ1136_A10.102"

/note="probably inactive due to 3' exon missing in CDS probably inactive due to 5' exon missing in CDS probably inactive due to including stop codon(s) in CDS pseudogene, maize retrotransposon Cinful-1 polyprotein*
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rarklagerrrfgtngghodyenvaanspardpdfspwaalbefpppgtedgaraqyrd
aadhivhsfegtaprlafaldsdeeggddgaddsddeagdpgase"
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13728. .15631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown protein"
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/db_xref="GI:38423961"
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/note="contains full-length cDNA(s): AK106729"
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/protein_id="BAD01669.1"
/db_xref="GI:38423960"
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/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="OJ1136_A10.103"
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'groduct="Nuclear inhibitor of PP1-like"
'protein_id="BAC22308.1"
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/gene="0J1136_A10.105"
/note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(joIn(36412. .36764,36875. .36967,37057. .37185,
37300. .37469,38065. .38266,38370. .38417,38684. .38779))
gene="OJ1136 Al0.108"
/note="supported by full-length cDNA(s): AK121204"
complement(join(36459. .36764,36875. .36967,37057. .37185,
37300. .37469,38065. .38266,38370. .38417,38684. .38776))
/gene="OJ1136 Al0.108"
                                                                                                                                                                                                                                                                                               37300. .37469,38065. .3
/gene="OJ1136_A10.108"
/note="contains EST(s):
                                                                                                                                                                                             D22533(C0190), C98574(E0421), C71831(E0421), D15164(C0190A)
contains full-length cDNA(s): AK121204, AK062210, AK098843"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37300. .37469,38065. .38266,38370. .38417,38684. .38775))
/gene="0J1136 Al0.108"
/note="energy for the state of the state 
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/gene="OJ1136_A10.108"
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TLRLSLVSGGDVHFSWWLRNGHRFNAECTERWLRVSATCPVCRDMPSSSPMATPLAEA
VPPLFWPKWKKKENKGERGKKKKGRR"
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LPSPPDFNDEDAVVAYNTI LNRYGI SKSDLSRSKDSSGDASGANDDNEFAGRPLKRSK
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lpqnshvgtsqshlspqgaslrvagqetgapghagtqvgggqgamqppdmaieprpgv
yylevlkdgdvidrinlekkrhifgrqvpacdfvldhqsvsrqhaavvphrngsivvi
                                                                                                                                                                                                                                                                                                                                                                                      /note="supported by full-length cDNA(s): AK098843"
complement(join(36633. .36764,36875. .36967,37057. .37185,
37300. .37469,38655. .38266,38370. .38417,38684. .38686))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="supported by full-length cDNA(s): AK062210"
complement(join(36476. .36764,36875. .36967,37057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="BAD01671.1"
/db_xref="GI:38423962"
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oin(27619. .27689,27815. .28820,28918. .30470,30553.
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psatfpapiyvæeerrwsinptelqeaakgneiwrsppllalpkfpgvdkpappisl
vllqpraqlvlpppsslallaptilllpshrinmchnsqivai"
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/product="60S ribosomal protein L7A"
/protein_id="BAD01672.1"
/db_xref="G1:38423963"
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protein_id="BAC22309.1"
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24393. .>24830
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Best Local Similarity
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1 CGUACUGCAACUCG 14
                                                                          Conservative
                                                                                                                                                                                                                   join(39419. .39600,39678. .39693)
                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mapkrggrapvpakkktekvtnplfekkpkgfgIggalppkkdl
hrfvkwpkvvrIgrgrrIlkgrlkvppalngptrtldknlatnlfkmllkyrpedkaa
kkerllkragabaegktveakkpIvvkyglnhvtylIegskaglvvIahdvdpIelvv
                                                                                                                                                                                                                                                                                                                    NDKFDEVRKKWGGGVMGSKSQAKTKAREKLLAKEAAQRMT"
                                                                                                                                                                                                                                                                                                                                                            WLPALCRKMEVPYCIVKGKARLGSIVHKKTASVLCLTTVKNEDKLEFSKILBAIKANF
                                                                                                                                                                                                                                             'gene="0J1136_A10.109"
                                                                      100.0%; Score 14; DB 15; Length 101249; 78.6%; Pred. No. 4e+03; tive 3; Mismatches 0; Indels 0;
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Sequence split into 64 fragments 700001 50000 300001 100001 LOCUS AE016853 Accession AE016853

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RESULT 9
CP000058 08/c
WPCOMMENT
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   Pragment Name CP0000058 01 CP0000058 03 CP000058 11 CP000058 13 CP000058 13 CP000058 22 CP000058 22 CP000058 23 CP000058 24 CP
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28 CGTACTGCAACTCG 97415
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CR954209 5/c
WPCOMMENT
Sequence split into 7
Fragment Name
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CR954209 4
CR954209 6
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LMFLCHR18 00
WPCOMMENT
LOCUS LMFLCHRIB 1091246 bp
DEFINITION Leishmania major strain Friedlir
Chr. 18, Chr. 19, Chr. 20, Chr. 22, ***
unordered pieces.
ACCESSION AL499620
VERSION AL499620.1 GI:11877283
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Pred. No. 4e+03;
3; Mismatches
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THE ORDER OF CONTIGS IS NOT KNOWN.
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NOTE: This is a 'working draft' sequence. It currently consists of 722 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                               This record will
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                                          gene
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                                                                                                                                                                                                                                                                                                                    Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(8-mail:teasakiamias.affrc.go.jp, URLinttp://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
Dec 2, 2003 this sequence version replaced gi:34328000.
Genes were predicted from the integrated results of the following:
(http://www.sciberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark.hmm), RiceHPM
(http://yrgp.dna.affrc.go.jp/RiceHPM/), SplicePredictor
(http://lgo.dna.affrc.go.jp/RiceHPM/), SplicePredictor
(http://lgo.dna.affrc.go.jp/RiceHPM/), SplicePredictor
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
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(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 133106)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group) genomic DNA, PAC clone:P0670E08.
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   complement (4155. .4698)
/gene="P0670E08.1"
                                                                                                                     /db_xref="taxon:39947"
/chromosome="8"
                                                                                                                                                                                       cultivar="Nipponbare"
                                                                                                                                                                                                                                  organism="Oryza sativa (japonica cultivar-group)"
ממס type="genomic ממא"
                                                                              clone="P0670E08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains full-length cDNA(s): AK108041
non-coding transcript
probably inactive due to including stop codon(s) in CDS"
join(15133. 15163,15236. 15327,16054. 16091,16202. 16
join(15133. 15163,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202. 16091,16202
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/gene="P0670808.2-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-coding transcript probably inactive due to including stop codon(s) complement (join(20758. ,22908,23398. .24423)) /gene="P0670E08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="supported by full-length cDNA(s): AK062314" complement(20190. .20643) /gene="P0670808.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gypsy type transposon-like" complement(20190. .20643) /gene="p0670E08.5"
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/gene="p0670E08.2-2"
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/translation="MARYAARWIYMALMMWAHDQKGASNSGEDLARQKGRVGGGSRWG
EARNENRGKABEIAVGGWGRRTAARCVGNIGGGRDASAALGAIGVGRGGCEDVVGGGR
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/gene="P0670E08.1"
                                                                              /note="hypothetical ORF
predicted by GENSCAN
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/gene="P0670E08.5"
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/gene="P0670E08.2-2"
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/gene="P0670808.1"
                                                                                                                                                                                   complement (join (28590. .28904, 29841.
                                                                                                                                                                                                                                                                 complement (join (28590 . . 28904, 29841.
                                                                                                                                                                                                                                                                                                                                        /note="probably inactive due to pseudogene, GAG-POL precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (24490.
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   this category is not included in IRGSP standard"
34966. .40113
                                                                                                                                                    /gene="P0670E08.8"
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/note="probeble:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0670E08.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="gypsy-type retrotransposon-like"
complement(24490. .26260)
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/gene="P0670E08.4"
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/gene="P0670E08.3"
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/codon_start=1
                                                                                                                                                                                                                                                                                                        'pseudo
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RESULT 17
AC044825/c
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AC044825 140409 bp DNA linea Homo sapiens chromosome 1 clone RP11-275I14 map SEQUENCE, 39 unordered pieces.
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Gakgroqtidskalmtawkaacaatgavtlulppgtyyigpvgphgdcskattmtplu
QGTILKAATILKREGRUMVEPGWVNHLIVSGQNGAAFDGQGAASWPPNKCBIRKDCKVL
PTSVLFVNNKNMVVQNVASVNSKFFHMALLQCSGAKISGVKISAPESSPNTDGIHIER
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I EVRNI EEFTWLNAS YS PVLKQLESQSMI DYY FRTHRANSDSNLKYRNPKYLS I LNHL
RFYLPEI Y PNLHKI VFLDDDVV I KKDLTSLMS I DMKGKV I GVVETCGES FHR FDR YLN
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RQR I REVQKVLGDASKDSDLÞKNANBKVKTLEQTLI KGKLMQDDCSVVVKKLRAMLHS
AEBQLHAHKKQTVFLTQLAAKTLÞKGLHCLÞLRLANBY FLLDÞSHQQFÞNKBKLDDÞK
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VRDMT FHGTMNGVR I KTWENS PTKSNAAHML FENLVMNDVQN PI I I DQKYCPYYNCEH
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/gene="P0670E08.10"
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join(35022. .35130,35266. .35300,35395. .35436,35536.
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35759. .35955,37221. .37465,37583. .37940,38024. .38599,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0670E08.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="start and end point are not identified"
join(47062. .47070,47132. .47626)
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|gene="P0670E08.11"
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protein_id="BAD03446.1"
db_xref="G1:38637195"
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contains full-length cDNA(s): AK069803"
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/gene="P0670E08.10"
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!VNQGRGVKASKLNALPLETVGSLKEPVGIVFSEESRESASKSTEPDSQEFLLRKAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 15; Length 133106; Pred. No. 3.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 27, 2000 this sequence version replaced gi:7543788. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pollara, V., Rogov, P., Rothman, P., Pollara, V., Rogov, P., Rothman, P., Rogov, P., Rothman, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Codege, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Gyette, M., Graham, L., Guerton, I.
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                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                          as soon as it
be preserved.
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Center clone name: 275_I_14
Center clone name: 275_II is contact to the contact to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.960731
Consensus quality: 120391 bases at least Q40
Consensus quality: 129577 bases at least Q30
Consensus quality: 133768 bases at least Q20
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Insert size: 136609; sum-of-contigs
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1156: contig of 1156 bp in length 1256: gap of 100 bp 2265: contig of 1009 bp in length
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15478: 15578: 17753:

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4946 7368 3677 4846

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AP005426
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Best Local Similarity 78.6%;
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Oryza sativa (japonica cultivar-group)
oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                         Oryza Bativa (japonica cultivar-group) PAC clone:P0668D04.

AP005426
                                                 AP005426.3 GI:50725953
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15579. .17753
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13793. .13892
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
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17854 19432 19432 211598 23137 23237 23237 236004 26004 26004 26004 233002 33002 33102 33102 33102 33102 33102 33102 33102 33102 34107 41171 4171 4117

gap of contig ga

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gene mRNA CDS	FEATURES	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT	
/or	(http://www.sci (http://www.ti (http://www.ti (http://globin. (http://globin. (http://globin. (http://www.ti (http://www.ti (http://www.ti (http://www.ti (http://www.ti genomic sequence database, nr (d sequence database, nr (d sequence) with the A gene with the Classified base such as same na significant hor EST homology (d sequence) is cloby two or more 'hypothetical' predicted by a a probable 'hyy predicted by a a probable 'hyy or or more o'hypothetical' predicted by a a probable 'hyy redicted by a a probable 'hyy		Ehrhartoideae; Oryzeae; Oryza.
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gene mRNA	mRNA misc_feature gene misc_feature gene mRNA mRNA	mRNA misc_feature gene misc_feature	
/protein id="BAD3482.1" /protein id="BAD3482.1" /db_xref="g1:50725955" /translation="MTVVVVADDAAAAAAQQQEELPEGHGQTVCVTGAAGYIASWLVELLERGYTVKGTVRNPDDEKNAHLKALDGADERLYJCKADLLDYDSIRAAVDGCHGVETTASBEVTDDEKQMVEBAVRGTEKVIKAAABAGTVRRVVTTSSIGAVTMDENRGEDVVVDESCWSDLEFCKKTKNWYCYGKAVAEQBACKAABERGVDLVVSPVLVVGPLLQPTVASAVHILKYLDGSAKKYANAVQAYVDVRDVAAHVRVFEADEAGRHLCAERVJHR EDVVHILGKLFEBYPVTTGCSDEVNPRKQPYKMSNKKLQDLGLHFIPVSDSLYETVKSLQEKGHLPVLSKEIPERLMCVPA" COMPIlement(join(1441415107,1552115709,1581415968, 1609916313)) /gene="P0668D04.4-2" complement(join(1441415107,1552115709,1581415968, 1609916313)) /gene="P0668D04.4-2" /note="confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /gene="p0668D04.4-2" /note="confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285)) /confilment(join(1475115107,1552115709,1581415968, 1609916285) /confilment(join(1475115107,1552115709,1581415968, 1609916285) /confilment(join(1475115107,1552115709,1581415968, 1609916285) /confilment(join(1475115107,1552115709,1581415968, 1609916285) /confilment(join(1475115107,1552115709,1581415968,		join(<27937588,77057793,7901>8340) /gene="P0668D04.2-7" /note="supported by full-length cDNA(s): AK121336 2793.	

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JOURNAL REFERENCE
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SOURCE
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AUTHORS
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                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                     вавакі, Т., Matsumoto, Т. and Katayose, Y.
Oryza sativa nipponbare(GA3) genomic DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP005429 I54950 bp DNA linear Oryza sativa (japonica cultivar-group) genomic DNA, PAC clone:P0701F11.
AP005429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP005429.3 GI:50252464
                                                                                    clone:P0701F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                 ished Only
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudogene, En/Spm-related transposon protein*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0668D04.7"
22537. .23576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mtvvvvaddaaaaaaaaaaqqqeelppghgqtvcvtgaagyiasml
vklilergytvkgtvanpdprahikaldgadelvlvlckadilysgtraavdgchg
vphtaspvtddpdgqwepavrgtevyikaaargdtyrvvytssigavtmdpragpdv
vvdescwsdlefckktknwycygkavabqeackaabergvdlvvvspvlvvgpllqpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASVGWVERTTGLAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="start and end point are not identified"
complement(join(17951. .18249,19523. .19577))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<17951. .18249,19523. .>19577))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0668D04.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDVVHILGKLFPEYPVPTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNASAVHILKYLDGSAKKYANAVQAYVDVRDVAAAHVRVFEAPEASGRHLCAERVLHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative cinnamoyl CoA reductase"
/protein_id="BAD33483.1"
/db_xref="GI:50725956"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0668D04.7"
/note="probably inactive due to 5' exon missing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAGGTAASPRGSCGGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="BAD33485.1"
/db_xref="GI:50725958"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="start and end point are not identified"
join(21544. .21564,21810. .21888,21992. .22077)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<21544. .21564,21810.
/gene="P0668D04.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="BAD33484.1"
/db_xref="G1:50725957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0668D04.5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAAQILEAGWFGGAGGRAGDERQAGRAAGVGGAGGAAATPGNAA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="predicted by GeneMark.hmm etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0668D04.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 14; DB 15; 78.6%; Pred. No. 3.8e+03;
in Database (2002)
154950)
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                                                                                                                  DNA,
                                                                                                                      chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 148848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLN 13-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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TITLE
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                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a probable 'hypothetical' protein and is include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jul 12, 2004 this sequence version replaced gi:38347824.

Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.sottberry.com/), GeneMark/), GlimmerM
(http://www.sottberry.com/), GeneMark/), GlimmerM
(http://www.sottberry.com/), GeneMark/), GlimmerM
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://rop.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://rop.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://slobin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://globin.cse.psu.edu/html/docs/si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (B-mail) tesaski@mise.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sasaki, T., Matsumoto, T. and Katayose, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JUN-2002) Takuji Sasaki, National Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                 /product="putative WIZZ"
/product="putative WIZZ"
/protein_id="BAD28643.1"
/db_xref="G1:5022465"
/db_xref="G1:5022465"
/translation="MDDDGDGSSSPTDDSAAAGLLPLFSRSPAEDLBEKLRRAMEENA
/translation="MDDDGDGSSSPTDDSAAAGLLPLFSRSPAEARBDAPARBDAPAA
STACPSRQQPFTABPRPRIVETVRVADAADAPADADANSMETVXDGYQMKYGQKVTRDN
STACRSFASCFVKKXLQRCAEDRSMLVATYBGEHNHALSTQTTEFVABGCTTS
PYPRAYFRCAFAPSCFVKKXLQRCAEDRSMLVATYBGEHNHALSTQTTEFVABGCTS
QHAGGSSSSPLPCSISINSSGRTITLDLTNQAGSGSIASCGVEAAAVSGELVTVLSPE
LRRHLVBEVVQVLKNDAFFVBAVTNAVARVVDQIPHIPVHL*
LRRHLVBEVVQVLKNDAFFVBAVTNAVARVVDQIPHIPVHL*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join(7738 .8259,8789 .8911,9006 .9338,9472 .9684))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement
9472. .955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7738. .9684)
/gene="P0701F11.1"
                                                                       join(11245. .11304,12099. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0701F11.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="supported by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Oryza sativa
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="contains full-length cDNA(s): AK067834"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="P0701F11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join (7843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 full-length cDNA(s): AK067834"
3. .8259,8789. .8911,9006. .9338,
                                          .18084)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://rgp.dna.affrc.go.jp/,
                                                                            .12681,16273. .16317
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="myloedraagadavaerggeheasrvpdergeakerevarprda 
vhnpprcrmelgrrlpktmmppppsfldfdwdeaakdegvgsgggdpaggrplrplve 
eaatorvgsdgsksvogikereeekvwaprmasglwlakfvskgvslan"
                                                                                                                                                                                                                                                                                                                                                                                     LFAKVARGRLTEEHARRYFQQLVAAVGFCHGRGVAHRDLKPENLLLDEEGRLKVTDFG
LAALFEQLRQDGLLHTQCGTPAYVAPSYLRKRGYDGARADLMSCGVVLYVLLCGFLPF
QHRMYAKMYGN IFKAEYQVPFWYSGDARRLI VRLLVVDPAKRISI PEIMRTPWFKKGF
QHRMYAKMYGN IFKAEYQVPFWYSGDARRLI RRLLVVDPAKRISI PEIMRTPWFKKGF
VPPVFTSPVSFKKWEEDDVLLDGGDSGAMSPRTCNAFQLISSMSGFDLSGMFESBQK
AATVFTSRAPAATVLQKLEAVGRSLGYSATRGKGWKLRLEATASVQRDVKSVGCISFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="supported by full-length cDNA(s): AK100881" complement(join(23977. .24090,24325. .25451)) /gene="P0701F11.5-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (23977. .25632)
/gene="P0701F11.5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (23977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical ORF predicted by GlimmerM
                        GFLPFQHENYAKMYQKIFKABYQVPPWVSGDARRLIVRLLVVDPAKRISIPEIMRTPW
                                                ARGGELFAKVARGRLTEEHARRYFQQLVAAVGFCHGRGVAHRDLKPENLLLDEEGRLK
VTDFGLAALPEQLRQDGLLHTQCGTPAYVAPEVLRKRGYDGARADLWSCGVVLYVLLC
                                                                                                    /translation="marrareeeadqverklvlgryelgrllgqgtfakvyygrdlrs
GESVAIKVIDKARLRRTEGMVEQLRREISIMRMVRHPNVVGIREVLASRARVFVVMBY
                                                                                                                                                                                                                                                           /note="contains EST(s): C98911(E3245),C98910(E3245)
contains full-length cDNA(s): AK061220,AK061493,AK100881"
                                                                                                                                                                                                                                                                                                                                       complement (24100. .25470)
                                                                                                                                                                                                                                                                                                                                                                     FFARGYVQAKSRDV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="supported by full-length cDNA(s): AK119760"
complement(join(24001. .24090,24325. .25281))
/gene="p0701F11.5-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="supported by full-length cDNA(s): AK061220"
complement(23977. .25511)
/gene="P0701F11.5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 this category is not included in IRGSP standard" 
18428. .18697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="supported by full-length cDNA(s): AK061493"
complement(23977. .25509)
/gene="P0701F11.5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0701F11.5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="hypothetical protein"
'protein_id="BAD28644.1"
'db_xref="GI:50252466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="P0701F11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0701F11.3"
|8428. .18697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(11245. .11304,12099. .12272,12615. .12681,16273. .16317,
,7030. .17142,17983. .18084)
                                                                                                                                                          protein_id="BAD28646.1"
db_xref="GI:50252468"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(23977. .24090,24325. .25451))
gene="P0701F11.5-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="start and end point are not oin(18788. .18922,18960. .19280) gene="P0701F11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(<18788. .18922,18960. .>19280)
|gene="P0701F11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="P0701F11.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="P0701F11.2"
                                                                                                                                                                                                                                                                                                                    gene="P0701F11.5-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MVEQLRREISIMRMVRHPNVVGIREVLASRARVFVVMEYARGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="putative CBL-interacting protein kinase"
protein_id="BAD28645.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="contains full-length cDNA(s): AK119760"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="predicted by FGENESH etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      category is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by GENSCAN
                                                                                                                                                                                                        putative CBL-interacting protein kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
BX088687
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
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                                                                                                                                    COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96909
                                                                                                                            Submitted (15-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirites: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 17, 2004 this sequence version replaced gi:37805616.
                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio
                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 173867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish DNA sequence from clone CH211-206I14 in
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BX088687.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BX088687
                                                                              Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                        Center code: SC
                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTACTGCAACTCG 96922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MDGWPQDTGGHATAVAVDGHEVSGPTSPDQTASLGNTCPRPIEF AAVQLQLQLQLQLAEVAVQFAASGQARNKEENDRRNPMWDAKLKFKRNTNASKAV"
join(37537...37679,39125...39152,39477...39751,39967...4012
//gene="p0701F11.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted by GeneMark.hmm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="start and end point are not identified"
join(32286. .32494,34154. .34241)
/gene="P0701F11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="start and end point are not identified"
join(25884. .26128,26275. .26290)
/gene="P0701F11.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="hypothetical ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(37537. .37679,39125.
/gene="P0701F11.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="hypothetical protein"
protein_id="BAD28648.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="P0701F11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(<25884. .26128,26275.
/gene="P0701F11.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /EALEVAADVAVVBFAHDAGDELEFNKFCAVDVRPGLADIVWAWQGDRPAAPDVAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="GI:50252470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="predicted by GENSCAN etc."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oin(<32286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="P0701F11.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MWRLIGPPCLPVWRDRLMTTWRVVVSLLLLPRAINLEVGTWKGG
IQILBAAARPYGRSTRVRLSSSGAPYFLRLGPGCDDWKVLM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="hypothetical protein"
protein_id="BAD28647.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:40994808
                                                                                                            -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xref="GI:50252469"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 15
Pred. No. 3.8e+03
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .32494,34154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173867 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not included in IRGSP standard"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .39152,39477. .39751,39967. .40129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .>34241)
                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 154950;
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linkage

group

VRT 29-JAN-2004

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Gaps

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Sg

SdC

mRNA gene mRINA

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mRNA gene mRNA gene gene

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REFERENCE
AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession mumbers given in the feature table with their source databases:

Em; EMBL; Sw., SWISSPROT; Tr., TRENEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononuclectide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73300 CGTACTGCAACTCG 73313
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
                                                                                                                                                                                   Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baca, B., Baca, B., Baca, B., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC108605
AC108605.4 GI:23195553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus clone CH230-267P22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson Lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CH211-206I14 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 188872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .173867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="CH211-206I14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14; DB 5; Length 173867; Pred. No. 3.7e+03; 3; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA linear 1
22, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2002
PROGRESS
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

TITLE

REFERENCE AUTHORS

JOURNAL

COMMENT

Center project name: Center clone name: C

Contact: hgsc-help@bcm.tmc.

Project Information name: CH230-267P22

Web site: http://www.hgsc.bcm.tmc.edu/

Center: Baylor College Center code: BCM

of Medicine

ORIGIN

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Egan, A., Becotto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., Frinley, M., Flagg, N., Forbes, J., Foster, M., Poster, M., Garza, M., Garza, M., Garza, M., Garza, M., Garza, M., Gerra, T., Garza, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevra, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Jackson, L., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Lovan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Lorensuheva, L., Loulseged, H., Lozado, R. J., Lu, X., Man, J., Lewis, L., Li, Z., Liu, J., Lorensuheva, L., Loulseged, H., Lozado, R. J., Lu, X., Man, J., Lewis, L., Li, Z., Liu, J., Lorensuheva, L., Loulseged, H., Lozado, R. J., Lu, X., Man, J., Lewis, L., Li, J., Liu, J., Lorensuheva, L., Loulseged, H., Lozado, R. J., Lu, X., Man, J., Lewis, L., Liu, J., Lorensuheva, J., Mantathe, M., Mahmoud, M., Malloy, K., Mangum, A., Martin, R., Marti
                              Sibmitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21737677.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
     shotgun sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 188872)
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          only
contigs will be indicated in the feature
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DEFINITION
ACCESSION
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                          REFERENCE
                                                                                                                                     SOURCE
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                                                                                                                                                               EYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
       AUTHORS
                                                                                                                    ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                       60100 CGTÁCTGCÁACTCG 60087
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CGUACUGCAACUCG 14
                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 218764)
                                                                                                                                     AC103229.5 GI:30578703
HTG; HTGS_PHASE2; HTGS_DRAPT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                       AC103229 21
Rattus norvegicus clone
AC103229
                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329 Consensus quality: 177756 bases at least Q40 Consensus quality: 179112 bases at least Q30 Consensus quality: 179978 bases at least Q20 Estimated insert size: 191240; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:RXAEL95TV"
complement(182094..182991)
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_end_extension clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:Sp6"
7946._.8460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estimated_length=unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="wgs_end_extension
lone end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="CH230-267F22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .18887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185765: contig of 185765 bp in length 185865: gap of unknown length 188872: contig of 3007 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xref="genomic DNA"
xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence:RXAEL95TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 14; DB 14; Length 188872; 78.6%; Pred. No. 3.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _end:Sp6
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Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
                                                                                                                                                                                                                           218764 bp DNA
ne CH230-217018, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                               WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                           near HTG 13-MAY-2003
DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Avalacesch, Alien, H., Alabocote, S., Jamin, A., Angulacesch, W., Aoya; A., Avgoliston, D.

Anyalecesch, W., Aoya; A., Avgolist, Bacas, Baden, H., Benahmed, F., Baladin, D., Bandaranalke, D., Barber, M., Barnetead, M., Benahmed, F., Biswalo, K., Biski, J., Blankenburg, K., Blych, B., Stone, A., Catter, K., Balar, J., Elankenburg, K., Blych, P., Brown, M., Chen, Y., Chen, Z., Chu, J., Chacker, M., Catter, K., Cavacos, J., Ceasar, H., Center, A., Chen, Y., Chen, Z., Chu, J., Checko, J., Chavez, D., Chan, R., Conter, A., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cookes, H., Core, A., Dedrin, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Cookes, H., Core, A., Dedrin, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cherko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cherko, J., Cherko, J., Chen, Y., Chen, Z., Chu, J., Cherko, J., Chen, Y., Chen, Z., Chu, J., Cherko, J., Chen, Y., Chen, Z., Chu, J., Chen, Y., Chen, Z., Chu, J., Chen, J.,
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REFERENCE AUTHORS TITLE JOURNAL

TITLE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                   Submitted (29-JAN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 29, 2005 this sequence version replaced gi:57863663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۳
  Center code:
Web site: ht
                                             Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 230865)
                                                                                                                                                                                                                                                                                                                       Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence
BX640547
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX640547 230865 bp DNA linear VRT 29-JAN-2
Zebrafish DNA sequence from clone DKEY-4J21 in linkage group 14,
                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                          Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                             BX640547.35 GI:58331761
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(see http://www.hggc.bcm.tmc.edu/docs/cenbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 218764: contig of 218764 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTACTGCAACTCG 170304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGUACUGCAACUCG 14
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Center clone name: CH230-217018

------ Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 211841 bases at least Q40

Consensus quality: 213096 bases at least Q30

Consensus quality: 213070 bases at least Q20

Estimated insert size: 218571; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor Co
Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10116"
/clone="CH230-217018"
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|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .218764
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78.6%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 218764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRT 29-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 24
AC021883/c
LOCUS
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                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ب
                                                                Direct Submission
                                                                                                                                                      The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGUACUGCAACUCG 14
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Contact: zfish-help@sanger.ac.uk
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: KMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submitted During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-4J21 is from a Zebzafish BAC library VECTOR: pIndigoBAC-5

/organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="DKEY-4J21" Location/Qualifiers /clone_lib="DanioKey"

Local Similarity Conservative 100.0%; ω --Score 14; DB 5; Pred. No. 3.6e+03; Mismatches 0, Length 230865; 0 Gaps

0

232180 bp DNA 1.
Homo sapiens chromosome 1 clone RP11-588H15,
PROGRESS ***, 40 unordered rianam linear 5, *** S r HTG 25-AUG-2000 SEQUENCING IN

BX640547 LOCUS

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Matches

ORIGIN

FEATURES

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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

SOURCE ORGANISM

KEYWORDS

VERSION ACCESSION DEFINITION

AC021883 AC021883.4 Homo sapiens (human) HTG; HTGS_PHASE1. GI:9910096

1 (bases 1 to 232180) Waterston, R.H. Hominidae; Homo. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;

Unpublished

2 (bases 1 to 232180) Waterston, R.H.

Submitted (21-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

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COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 181000; agarose-fp
Insert size: 228280; sum-of-contigs
Quality coverage: 6.35 in Q20 bases; agarose-fp
Quality coverage: 4.69 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; 14%
Chemistry: Dye-primer ET; 86% of reads
Chemistry: Dye-terminator Big Dye; 14% of rea
Assembly program: Phrap; version 0.990319
Consensus quality: 211766 bases at least Q40
Consensus quality: 21799 bases at least Q20
Consensus quality: 221643 bases at least Q20
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----- Summary Statistics
Sequencing vector: M13; 86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is
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|mol_type="genomic DNA"
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                                Submitted (21-JAN-2003) Max Planck Institute for Molecular Genetics, proScience Ihnestrasse 73, D-14195 Berlin, Germany Max Planck Institute for Marine Microbiology Celsiusstrasse 1, D-28359
                                                                                                                                                                                                                                                                     1 (bases 1 to 293350)
Glockner, F.O., Kube, M., Bauer, M., Teeling, H., Lombardot, T.,
Glockner, F.O., Kube, M., Borzym, K., Heitmann, K., Rabus, R.,
Ludwig, W., Gade, D., Beck, A., Borzym, K., Heitmann, K., Rabus, R.,
Schlesner, H., Amann, R. and Reinhardt, R.
Complete genome sequence of the marine planctomycete Pirellula
                                                                                                                                                                                                                                                                                                                                                                      Rhodopire Iula baltica SH 1
Rhodopire Iula baltica SH 1
Rhodopire Iula baltica SH 1
Bacteria, Planctomycetes, Planctomycetales,
Planctomycetaceae; Rhodopire Ilula.
                                                                                                              Kube,M., Borzym,K., Heitmann,K., Klages,S., Marquardt,I.,
Lehrack,S., Beck,A., Pawlik,R., Reinhardt,R., Gloeckner,F.
Bauer,M., Teeling,H., Lombardot,T., Ludwig,W., Gade,D., Ra
Schlesner,H. and Amann,R.
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BX294153.1 GI:32447383
                                                                                               Direct Submission
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Pirellula sp. strain 1 complete
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20769. .22399
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22400. .22499
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17006. .18051
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13643. .14982
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18152. .19373
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12304. .13542
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12204. .12303
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Planck Institute for Marine Microbiology, Bremen, German fremework of the REGX-project, http://www.regx.de
                                                                                        *Max Planck Institute for Molecular Genetics, Berlin, Germany;
                                              Germany; in the
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Center: Max Planck Institute for Molecular Genetics Center code: MPIMG

Sequencing vector: pUC19; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 7142841 bases at least Q30 Consensus quality: 7145484 bases at least Q30 Quality coverage: 8.03 of reads

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or coveredby high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; allregions were covered by at least one plasmid Sequence; assembly was additionally confirmed by long range pcr and cosmid end sequences.

See http://www.micro-genomes.mpg.de/pirellula/ for more information including minimal tiling path from a set of 220 cosmids out of 908. See the misc_feature tag below for the boundaries of the MTP COSMICS.

ds. ----- Annotation
Center: Max Planck Institute for Marine Microbiology

Center Code: MPIMM Celsiusstrasse 1, D-28359 Bremen, Germany

Phone: fog@mpi-bremen.de +49 (0)421 2028 938 Fax: +49 (0)421 2028 580

Three different programs (Glimmer, Critica and Orpheus) were used for ORF-prediction. A nonredundant list of ORFs was generated by suitable parsing of the results.

Automated annotation was done with the software package Pedant Pro (http://www.biomax.de). All ORF predictions and annotations were manually corrected by considering all results of the different tools applied. See http://www.regx.de for more information and access to supplementary information.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                               /Tocus_tag="RB11183"
//note="PMID: 9371463 best DB hits: BLAST: pir:A69220;
/note="PMID: 9371463 best DB hits: BLAST: pir:A69220;
/note="PMID: 9371464 protein MTH898 - Methanobacterium;
E=1e-07 gb:AAD46412.1; AF096262 1 (AF096262) ER6 protein
[Lycopersicon; E=1e-05 gb:AAR04173.1; AB006246 3
[AB006246) conserved hypothetical; E==05 COG: MTH898;
COG0589 Universal stress protein UspA and related; E=1e-08
PFAM: PF00582; Universal stress protein family; E=4e-11"
/db_xref="InterPro:IPR006016"
/db_xref="UniProt/TrEMBL:G/UER2"
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/translation="MRVLLAVDSSPYSQQAVEFASHLPLRKPVDFDLVSVVAPPMLVD
TGGMSMPMDF05FLEIETDRSREAIDAVASDLKSQDHVHSVHTHVPIGPPTSALLDVA
DESGADLIVLGAIGHSAIERVLLGSVSDYVATHADMSTLVVRPTSEADVEPDLQKIML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="RB11183"
complement(93. .1040)
                                                                                                                                                                                        /product="conserved hypothetical protein"
/protein_id="CAD78973.1"
/db_xref="GI:32447384"
                                                                                                                                                                                                                                                                                                     /codon_start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:243090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rhodopirellula
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="
                                                                                                                                                                xref="GOA:Q7UER2"
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gene

gene

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.4012)

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/locus tag="RB11186"
/function="two-component signal transduction"
/function="two-component signal transduction"
/note="best DB hits: BLAST: gb:AAG45333.1; AF273214_1
/AF273214) SasR [Myxococcus xanthus]; E-3e-83
swissprot:Q06065; ATOC_ECOLI ACETOACETATE METABOLISM
REGULATORY; E-1e-81 gb:AAC28085.1; (AF100457) response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLFSRVVIAISNAESDTALPDWVAALRLVPNCEVHLVHVMETHPEYELHLLKKVAAYM
BEVRSAAWKLMETTRPRLBALGMKVKPSLLESPHVGRAVLEYANEHACDLIVVGDQDD
SLMERVMLGSVSRFVVRHANQSVLIVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNERNGPKLRTLIGIDSSAPARDALQALSKSTLAEACEVSLATI
VPEPPLYTIDDTSMPWIPQEVFDSRLEIENTQLKQLQQEFGERFSSCEFSVSQGHPGR
GLIEMSERFDADWIVIGSVGHSAFSRILLGSTSDYVANRSTRTCLVHRPITTDHEPSK
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/locus_tag="RB11184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQILDFETKLQQLGLNTETHFVESNHVGETLVEYARRHGCDLAVTGDSDSGLLTRVFL
GSTSRYVLRHADCSVLIIRDREDRAKAHRQIAEQSLAST"
                                                                                                                                                                                                                                                                                                                                                                                                                                           regulator [Myxococcus xanthus]; E=5e-80 COG: atoC; COG2204
AAAA superfamily ATPases with N-terminal receiver; E=1e-82
PFAM: PF00072; Response regulator receiver doma; E=2.7e-32
PFO0158; Sigma-54 interaction domain; E=1.1e-119"
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/db_xref="UniProt/TrEMBL:Q7UEQ9"
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/translation="MIGITMSQTAIKYLLVDDEDDYRRSCGKEMERMGHTVRLAASGA
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EAMSFLDREAFDVAVFDIDMFGMSGLELMQRVHEESHDVEVVFLTGKGTIEACVQAMQ
EAMSCDFLTKECSLADLEHRVGLAQQBGHLKKENQQLKAIVHRWRESFKLIGMSLAMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (2139. .3614)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         universal stress protein
/protein_id="CAD78975.1"
/db_xref="GI:32447386"
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                                                                                                                                                                                                                                                                                                  'product="NtrC-like response regulator SasR"
'protein_id="CAD78976.1"
'db_xref="GI:32447387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omplement (2139. .3614)
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7531_METJA HYPOTHETICAL PROTEIN MJ0531 ----; E=7e-04 COG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="PMID: 8905231 best DB hits: BLAST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locus_tag="RB11185"
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/translation="MFASRWTWVRAASLTASPTCATPSHLARHSQQNASWSEPCK"
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protein_id="CAD78974.]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amily; B=0.04"
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codon_start."
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L11388; E=2e-05 gb:AAG20091.1; (AE005088) Vng1898c
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                                                                                                                                                                                            _xref="InterPro:IPR002078"
_xref="InterPro:IPR002197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xref="InterPro:IPR006016"
xref="UniProt/TrEMBL:Q7UER0"
                                                                                                                                                                                                                                                    xref="InterPro: IPR001789"
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                                                                                                                                                                                                                                                                           xref="GOA:Q7UEQ9"
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RESULT 27
AX988576/c
LOCUS
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ORGANISM
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CQ554118
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KEYWORDS
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Best Local S
Matches 10
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TITLE
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                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                           31
                                                                                                                                                                                                                                                    10;
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Sequence 23753 from Patent CQ554118 CQ554118.1 GI:41520545
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AX988576
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                                                                                                                                                                                                                                                                                                                                                       Compugen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="unassigned DNi
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db¯xref="UniProt/TrEMBL:Q7UEQ8"
/translation="MIEISHGARRQRNGNNITSPFVILKIRASITRSHRERHAMLLFV
TPPLNPTCENSRPILHRSIRFDADVVTGLFTDRFAGCFHAPRPAVP"
                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="two-component signal transduction"
/note="PMID: 2666400 PMID: 11243806 best DB h:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="hydH"
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'BC_number="2.7.3.-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="hypothetical
protein_id="CAD78977.1
db_xref="GI:32447388"
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76.9%;
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                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14; DB 1;
Pred. No. 3.5e+03;
3; Mismatches 0
                                                                                                                                                                                     Score 13; DB 6;
Pred. No. 3.3e+04;
 100
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mintz, B., Mintz, L. and Faigler, S.
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                                                                                                                                                                                                         Length 65
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 PAT 16-JAN-2004
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RESULT 29
AF069774
LOCUS
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AUTHORS
TITLE
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SOURCE
ORGANISM
                                 ACCESSION
VERSION
KEYWORDS
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AUTHORS
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ORGANISM
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ACCESSION
VERSION
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VERSION
KEYWORDS
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AX988577/c
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                                                                     DEFINITION
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             ORGANISM
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                                                                                                                                         52
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                                             Mus musculus chapsyn-110 mRNA, AF069774 AF069774.1 GI:3335542
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AX988577
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Escherichia coli
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Mus musculus
Bukaryota; Me
                        Mus musculus (house mouse)
                                                                               AF069774
                                                                                                                                                                                                                                                                                                                                      Biochip
                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent: EP 1260592-A 39 27-NOV-2002;
MWG -Biotech AG (DE)
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Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                 Patent: EP 1260592-A 40 27-NOV-2002;
MWG -Biotech AG (DE)
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                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="yojh b2211 U00096 complement(2303128__2304774)"
                                                                                                                                                                                                                                          /organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="yojh b2211 U00096 complement(2303128__2304774)"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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 Metazoa;
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Chordata;
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Pred. No. 3.1e+04;
3; Mismatches 0
                                                                                                                                                                                    Pred. No. 3.10
3; Mismatches
                                                                                                                                                                                               Score 13; DB 6;
Pred. No. 3.1e+04;
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BP1260592.
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                                                                              186 bp
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Craniata; Vertebrata;
                                                                    partial cds
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 Euteleostomi;
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TRBPRTKNB/c
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2 GUACUGCAACUCG 14
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Submitted (03-JUN-1998) Anatomy, Hokkaido University
Medicine, N15W7, Kita-ku, Sapporo 060-8638, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei clone
L10992
                                                                                                                                                                                                                                                                        Original source text:
                                                                                                                                                                                                                                                                                                                                              Hua, S.B. and Wang, C.C.
Differential accumulation of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse chapsyn-110 partial cDNA Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma.
1 (bases 1 to 200)
                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                          rypanosoma brucei
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GTACTGCAACTCG 158
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             /note="putative"
/codon start=1
/product="protein kinase"
/protein id="AAA19804.1"
/db_xref="GI:310959"
                                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="chapsyn-110"
/protein id="AAC27299.1"
/db_xref="GI:3335543"
/translation="vyktCDKPASPRHYSPVBCDKSFLLSTPYPHYHLGLLPDSDMTS
HSQHSTATRQPSVTLQRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="channel-associated protein of synapse-110; similar
to Rattus norvegicus chapsyn-110 encoded by GenBank
Accession Number U49049 (Neuron, 17, Kim et al., 1996)"
                                                                                                                                                                               /organism="Trypanosoma
/mol_type="mRNA"
/strain="TREU667"
                                                                                                                                                                                                                                                    source text: Trypanosoma brucei
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:310958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
                                                                                                         dev_stage="blood stream;1...>200
                                                                                                                                               /db_xref="taxon:5691"
/clone="TbPK-A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="PCR-amplified fragment"
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translation="RDLKLDNIMMDANMNVKIRDFGLAAELQYDGERKRTICGTPNYI"
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TbPK-A2 protein kinase mRNA, partial
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2.9e+04;
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AY011660/c
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                                                                                                                  AY011660 398 bp Ateles fusciceps cAMP responsive partial cds.
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Ateles fusciceps (brown-headed spider monkey)
Ateles fusciceps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
Cebidae; Atelinae; Ateles.
1 (bases 1 to 398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-FEB-2000) Laboratory of Immunogenetics, Parklawn Drive, Rockville, MD 20852, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han, M., Nhu, Q., Folley, S. and Robinson, M.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleo
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta
                                                                                           AY011660.1
                                                                                                         AY011660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (rhesus monkey)
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                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="T-cfl receptor alpha chain"
/protein_id="AAF42931.1"
/db_xref="61:7239665"
/translation="MVLKFSVSILWIQLAWVSTQQLEQSPRFLSIQEGENFTAYCNSS
SVFTSLQWYRQDPGEGPVLLVTLVTRGEMKKQKRLTFQFGDARKDSSLHITATQPGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APEIIEGSREGHSYEVDVWAFGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="MMAV10-1"
                                                                                          GI:12699921
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Pred. No.
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Pred. No.
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Mismatches 0
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710-1 T-cell receptor alpha
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AUTHORS
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Submitted (01-NOV-2000) Laboratory of Genomic Diversity, National
Cancer Institute-FCRDC, P.O. Box B, Bldg. 560, Rm. 11-10,
                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta
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Molecular phylogenetics and the origins of placental mammals
Nature 409 (6820), 614-618 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACTCRAAL
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell receptor alpha.
Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                                                                                         Macaca mulatta TCR alpha chain sequences
Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAL 406 mulatta (clone VA1089)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CREM"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Ateles fusciceps"
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                                                                                                                    gene="TCR A"
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76.9%;
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Pred. No. 2.7e+04
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) T-cell receptor alpha
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RESULT 35
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AUTHORS
TITLE
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MACTCRAAK
      SOURCE
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VERSION
                                                   ACCESSION
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                    KEYWORDS
                                   VERSION
                                                                                DEFINITION
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Best Local S
Matches 10
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Best Local Similarity
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AK111239
AK111239.1 GI:32996448
FLI_CDNA; oligo capping.
Oryza sativa (japonica c
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Macaca mulatta (clone VA101)
end of cds.
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                                                                            Oryza sativa (japonica cultivar-group)
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T-cell receptor alpha.
Macaca mulatta (rhesus monkey)
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                                                                insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta TCR alpha chain sequences
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                                                                                                                                                                                                                                                                                                             /translation="MVLEFSVSILWIQLAWVSTQQLEQSPRFLSIQEGENPTAYCNSS
SVFTSLQWYRQDPGEGPVLLVTLVTRGEMKKQKRLTFQFGDRRKDSSLHITATQPGDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYLCAGVRINNDIRFGAGTRLTVGPNIQNPDP"
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                                                                                                                                                                                                                                                                                                                                                                                                                        gene="TCR A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="TCR A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="TCR A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Macaca mulatta"
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76.9%;
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Pred. No. 2.7e
3; Mismatches
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Pred. No. 2.7e+04;
   cultivar-group)
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receptor alpha
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                                                                                            PLN 24-JUL-2003
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A) mRNA, 5'
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PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirasoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Nagata, T., Koyima, K., Namiki, T., Ishikawa, M., Yamada, H., Ooka, H., Hotta, T., Koyima, K., Namiki, T., Ohneda, B., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
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Science 301 (5631), 376-379 (2003)
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JOURNAL
PUBMED
REFERENCE
AUTHORS
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SOURCE
ORGANISM
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ACIDOVOTAX 8p. A-07-20 16S ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Myazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (26-UUL-2002) Department of Microbiology, Microbiology and Immunology, 300-6174 University Blvd., Vancouver, BC V6T 1Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Briksson,M., Sodersten,B., Yu,Z., Dalhammar,G. and Mohn,W.W. Degradation of Polycyclic Aromatic Hydrocarbons at Low Temperature under Aerobic and Nitrate-Reducing Conditions in Enrichment Cultures from Northern Soils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acidovorax sp. A-07-20
Acidovorax sp. A-07-20
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Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 615)
Sodersten, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY136528.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACTGCAACTCG 193
                                       GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 615)
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Environ. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                 /product="16S ribosomal RNA"
                                                                                                                                                                                                                                                                                                           organism="Acidovorax sp. A-07-20" mol_type="genomic DNA"
                                                                                                                                                                                                                          note="aerobic PAH enrichment culture at 7 deg
                                                                                                                                                                                                                                                country="Canada: Alert"
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                                                                                                 92.9%;
76.9%;
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76.9%;
                                                                                                 Score 13; DB 1;
Pred. No. 2.5e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 15;
Pred. No. 2.6e+04;
3; Mismatches 0
                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NA linear BCT 07-JAN-2003
RNA gene, partial sequence.
                                                                                                                       Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 580;
                                                                              Indels
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                                                                              <u>,</u>
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RESULT 37

Query Match

92.9%; Score 13;

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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes verus
Pan troglodytes verus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNOS(30,25) (single strand NQS, the base in question has Phred score >= 30, the surrounding :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hgl6,July 2003). Chimp WGS reads were from 9 donors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jaffe, D.B.
Initial Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mikkelsen, T.S., Hillier, W.L., Bichler, B.E., Zody, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tagged site.
                                                                                                                                                                                                                     of human genome) were discarded.
                                                                                                                                                                                                                                                                                           copies of a single read, comparisons between two reads that share 95% of their genome
                                                                                                                                                                                                                                                                                                                                             than 100 NQS bases or with SNP rate exclude alignment between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score >= 25), and the read must have at least 200 bp SNQS(30 bases. Reads not uniquely placed in the genome and read pairs whose two ends were not
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                                                                                                                                                                                                                                               placed at the same locus
                                                                                                                                                                                                                                                                                                                                                                                                                        overlapping reads to call NQS bases and SNPs. Alignments (between .
                                                                                                                                                                                                                                                                                                                                                                                                                                                o all pairs of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roglodytes verus), 3 other Pan troglodytes verus chimps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3mail: mczody@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Pan.
1 (bases 1 to 620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              onsistently placed were
                                                                                                                                                                                                                                                                      ignments (>=95% bases of read A and >=95% bases of read B were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown origin
                                                                                        /organism="Pan troglodytes
/mol_type="genomic DNA"
/sub_species="verus"
                                              clone
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                                                                                                                                                                                                                                                                                                                                                                                         with less
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                                                                      xref="taxon:37012"
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>620
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                                                                                                                                                 verus"
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                                                                                                                                                                                                                                                                                                                                                                         0.01
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ORGANISM
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BV507671/c
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VERSION
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                                                                                                                                                                                                                                                                        western chimp and Pan
troglodytes troglodytes is the central chimp. To be included in
chimpanzee SNP discovery, a
read must be at least 500bp in length, at least 50% of its base
calls must have Phred
score >= 20, at least 30% of its base calls must satisfy
SNQS (30,25) (single strand NQS, the
base in question has Phred score >= 30, the surrounding 10 bases in
the read have Phred
score >= 25), and the read must have at least 200 bp SNQS (30,25)
bases. Reads not uniquely
placed in the genome and read pairs whose two ends were not
consistently placed were
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                                                                                                      overlapping reads to call NQS bases and SNPs. Alignments (between two reads) with less than 100 NQS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two copies of a single read, comparisons between two reads that share 95% of their genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gft62a12.g1 Clint Pan troglodytes verus STS genomic, sequence tagged site.

BV507671
                                            alignments (>=95% bases of read A and >=95% bases of read B were placed at the same locus of human genome) were discarded.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 693)
Mikkelsen,T.S., Hillier,W.L., Bichler,B.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes verus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
                                                                                                                                                                                                                                                      discarded. After above filtering, NQS(30,25) standard was applied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of unknown origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BV507671.1 GI:62351413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: No sequence submitted 
Primer B: No sequence submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               troglodytes verus), 3 other Pan troglodytes verus chimps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes verus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Gon, Unknown Chimp). Common names: Pan troglodytes verus is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prococol
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                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.9%;
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3; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                       30, the surrounding 10 bases
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ORIGIN
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DEFINITION
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Pan.
1 (bases 1 to 742)
Mikkelsen, T.S., Hil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes troglodytes
Pan troglodytes troglodytes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence tagged
BV635227
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S217P6390RB2.TO
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                                                                                                                                                                                                                                                                                                                                          of unknown origin
(Gon, Unknown Chimp). (
western chimp and Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2005)
                                                           score >= 25), and the read must have at least 200 bp SNQS(30,25) bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were consistently placed were discarded. After above filtering, NQS(30,25) standard was applied discarded. After above filtering, NQS(30,25)
                                                                                                                                                                                                                calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNQS(30,25)(single strand NQS, the
                                                                                                                                                                                                                                                                              troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23,021,928 chimpanzee whole genome shotgun reads were aligned the Human genome NCBI
Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors, including Clint (Pan
overlapping reads to call NQS bases and two reads) with less
                                              to all pairs of
                                                                                                                                                                                                                                                                                                                                                                                                                             troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer A: No sequence submitted
Primer B: No sequence submitted
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                                                                                                                                                                      the read have Phred
                                                                                                                                                                                          base in question has Phred score
                                                                                                                                                                                                                                                                                                                                                                                                           troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STS size: 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mczody@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 6172580903
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/mol_type="genomic DNA"

/sub_species="verus"

/db_xref="taxon:37012"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:62625405
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76.9%;
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Bite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, W.L.,
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
2.5e+04;
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                                                                                                                                                                                              30,
                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes verus is the
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                          SNPB.
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Catarrhini;

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STS 15-APR-2005 STS genomic,

Alignments (between

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JOURNAL COMMENT
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BV530657
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
  calls must have Phred score >= 20, at least 30% of its base calls must satisfy snos(30.25)(single strand NQS, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G591P617906RE7.T0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            copies of a single read, comparisons between two reads that share
                                                                                chimpanzee SNP discovery, a read must be at least 500bp in length,
                                                                                                                                                                                                    troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Genome
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 768)
Mikkelsen,T.S., Hillier,W.L., Bichler,B.B.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BV530657.1 GI:62408441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       than 100 NQS bases or with SNP rate > 0.01 were discarded. exclude alignment between two
                                                                                                                                                                                                                                                                                     the Human genome NCBI
Build 34 (hg16,July 2003). Chimp WGS reads were from 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes verus
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                                                                                                                                                                                                                                                                      ncluding Clint (Pan
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                                                                                                                                                                                     unknown origin
                                                                                                                                                                                                                                                                                                                                                                                                                                   : mczody@broad.mit.edu
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:1. .>742
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|mol_type="genomic_DNA"
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                                                                                                                         troglodytes is the central chimp. To be included in
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_xref="taxon:37011"
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Phred score >= 30, the surrounding 10 bases in
                                                                                                                                                             Common names: Pan troglodytes verus is the
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Pred. No.
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Pan troglodytes verus STS
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2.5e+04;
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                                                                                   at least 50% of its
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                                                                                                                                                                                                                                                                        Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA (
Tel: 617280933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes verus
Pan troglodytes verus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the read have Phred
score >= 25), and the read must have at least 200 bp SNQS(3)
bases. Reads not uniquely
placed in the genome and read pairs whose two ends were not
                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BV530662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies of a single read, comparisons between 95% of their genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           than 100 NQS bases or with SNP rate > 0.01 were discarded. To exclude alignment between two
(Donald, Karlien, Yvonne), 3 Pan
troglodytes troglodytes chimps
                                                                             the Human genome NCBI
Build 34 (hg16, July 2003). Chimp
                                                                                                                                                        rimer A: No sequence submitted
Primer B: No sequence submitted
375 size: 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BV530662.1 GI:62408446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            placed at the same locus
                                           troglodytes verus), 3 other Pan troglodytes verus chimps
                                                                                                                          23,021,928 chimpanzee whole genome shotgun reads were aligned to
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mikkelsen, T.S., Hillier, W.L., Bichler, B.B., Zody, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liscarded.
                                                              ncluding Clint (Pan
                                                                                                                                                                                                                                mail: mczody@broad.mit.edu
                                                                                                                                                                                                                                                     ax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                  initial Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    łominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACTGCAACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome) were discarded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lil
<1. .>768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pan troglodytes/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sub_species="verus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               After above filtering, NQS(30,25) standard was applied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (>=95% bases of read A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:37012"
ne_lib="Clint"
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76.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp DNA linear troglodytes verus STS
    (Noemie, Masuku, Clara) and 2 chimps
                                                                                      WGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 >=95% bases of read B were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic
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BV530664
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711
                                                                                                                                                                                                   Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            troglodytes troglodytes is the central chimp. To be included in chimpanzee SNP discovery, a read must be at least 500bp in length, at least 50% of its base calls must have Phred score >= 20, at least 30% of its base calls must satisfy SNQS(30,25) (single strand NQS, the base in question has Phred score >= 30, the surrounding 10 bases the same of the
Primer A: No sequence submitted Primer B: No sequence submitted STS size: 774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bases. Reads not uniquely placed in the genome and read pairs whose two ends were not consistently placed were discarded. After above filtering, NQS(30,25) standard was applied
                                                                                                                                                                                                                                                                                                                                                       Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 774)
Mikkelsen, T.S., Hillier, W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes verus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G591P617902RE6.TO Clint Pan troglodytes verus STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placed at the same locus of human genome) were discarded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlapping reads to call NQS bases two reads) with less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the read have Phred score >= 25), and the read must have at least 200 bp SNQS(30,25)
                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to all pairs of
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                                                                                                            Email: mczody@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jaffe, D.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes verus
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                                                                                                                                                                                                                                                                                                                                                                                                                           initial Sequence of the Chimpanzee Genome and
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<1. .>773
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/mol_type="genomic DNA"
/sub_species="verus"
/db_xref="taxon:37012"
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                                                                                                                                                                                                                                                                                                                                                                                                                        Comparison with
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                                                                                                                                                                                                                                                                                                                     ACCESSION
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                     JOURNAL
PUBMED
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                 ORGANISM
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8666794
2 (base
                                                                                                                                                                                                                  Myxine glutinosa (Atlantic hagfish)
Myxine glutinosa
Myxine glutinosa
Bukarrot
                                   Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes; Myxinidae; Myxininae; Myxine.

1 (bases 1 to 939)
Kandil, B., Namikawa, C., Nonaka, M., Greenberg, A.S., Flajnik, M.F., Ishibashi, T. and Kasahara, M.
Isolation of low molecular mass polypeptide complementary DNA clones from primitive vertebrates. Implications for the origin of MHC class I-restricted antigen presentation
MHC class I-restricted antigen presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlapping reads to call NQS bases and SNPs. two reads) with less than 100 NQS bases or with SNP rate > 0.01 we
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score >= 25), and the read must have at least 200 bp SNG
bases. Reads not uniquely
placed in the genome and read pairs whose two ends were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    score >= 20, at least 30% of its base calls must satisfy SNQS(30,25)(single strand NQS, the base in question has Phred score >= 30, the surrounding 10 bases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             placed at the same locus of human genome) were discarded
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Build 34 (hg16,July 2003). Chimp WGS reads were from 9 donors,
including Clint (Pan
                                                                                                                                                                                                                                                                                               D64054.1 GI:1405320
                                                                                                                                                                                                                                                                                                                                        Myxine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copies of a single read, comparisons between 95% of their genome
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discarded. After above filtering, NQS(30,25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Donald, Karlien, Yvonne),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignments (>=95% bases of read A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exclude alignment between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to all pairs of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   troglodytes troglodytes is the central chimp. To be included in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     western chimp and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of unknown origin
(Gon,Unknown Chimp). Common names:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23,021,928 chimpanzee whole genome shotgun reads were aligned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTACTGCAACTCG 719
  (bases 1 to 939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                      939 bp mRNA glutinosa mRNA for LMPX of hagfish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes
/mol_type="genomic DNA"
/sub_species="verus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:37012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone lib="Clint"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>س</u>
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             were discarded.
                                                                                                                                                                                                                                                                                                                                        complete
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                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two reads that share
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard was applied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignments (between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 bp SNQS (30,
                                                                                                                                                                                                                                                                                                                                                              VRT
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BV550217
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BV550217 971 bp DNA linear STS 09-APR-2005 S215P60320RD6.T0 Clara Pan troglodytes troglodytes STS genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GUACUGCAACUCG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-SEP-1995) Masanori Kasahara, Hokkaido University School of Medicine, Biochemistry; Kita 15 Nishi 7, Sapporo, Hokkaido 060, Japan (Tel:011-706-5047, Fax:011-717-5286) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
23,021,928 chimpanzee whole genome shotgun reads were aligned to the Human genome NCBI
Build 34 (hgl6,Jully 2003). Chimp WGS reads were from 9 donors, including Clint (Pan
                                                                                                                                                                                                            Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                             Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 971)
Mikkelsen, T.S., Hillier, W.L., Bichler, B.E., Zody, M.C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tagged site.
BV550217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BV550217.1 GI:62441237
                                                                             Protocol:
                                                                                               STS size: 971
                                                                                                                Primer A: No sequence submitted Primer B: No sequence submitted
                                                                                                                                                       Email: mczody@broad.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                fominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                  Genome
                                                                                                                                                                                                                                                                                                                                Sequence of the Chimpanzee Genome and Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEBAYDLGRRAICHATHRDAYSGGVVNLYHMQQSGWIKVSQNDVSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGLDPVEFLKPFASGESDVKIEFHHGTTTLAFKFDHGVIVAVDSRATAGSYVASQTVK
KVIEINPYLLGTMAGGAADCMYWERVLSKHCRIYBLRNKERISVAAASKLLANMVYQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="LMPX of hagfish"
/protein_id="BAA10931.1"
/db_xref="GI:1405321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="'mature LMPX of hagfish'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223. .831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MALAEVCGYREIAARLPRLEHRRECFGELQEALGGLHEQSFAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue type="Liver blood cell" clone_lib="Uni-ZAP XR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Myxine glutinosa"
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76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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R P P P R S
                                                                                              transformant containing the vector and process for producing formate dehydrogenase by using the transformant patent: JP 2000245471-A 1 12-SEP-2000; UNITIKA LTD
                                                                                                                                                                                                                                                                                                                                                                                                       Formate dehydrogenase gene, recombinant vector cont
transformant containing the vector and process for
formate dehydrogenase by using the transformant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        placed at the same locus of human genome) were discarded.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copies of a single read, comparisons between two reads that share 95% of their genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         troglodytes verus), 3 other Pan troglodytes verus chimps (Donald, Karlien, Yvonne), 3 Pan troglodytes troglodytes chimps (Noemie, Masuku, Clara) and
                                                                                                                                                                                                          1 (bases 1 to 1197)
Mitsunaga, T., Tanaka
                                                                                                                                                                                                                                                                                             Hyphomicrobium sp. Hyphomicrobium sp.
                                                                                                                                                                                                                                                                                                                                             JP 2000245471-A/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                than 100 NQS bases or with SNP rate > 0.01 were discarded. exclude alignment between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        overlapping reads to call NQS bases and SNPs. Alignments (between two reads) with less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score >= 25), and the read must have at least 200 bp SNQS(30,25)
bases. Reads not uniquely
placed in the genome and read pairs whose two ends were not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNQS(30,25)(single strand NQS, the base in question has Phred score >=
                                                                                                                                                                                          Formate dehydrogenase gene, recombinant vector containing the same,
                                                                                                                                                                                                                                                                                                                                                               E38273.1 GI:18626965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calls must have Phred
                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Hyphomicrobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to all pairs of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chimpanzee SNP discovery,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gon, Unknown Chimp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     core >= 20, at least 30% of its base calls must satisfy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roglodytes
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                                    Hyphomicrobium sp. JP 2000245471-A/1 12-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes
/mol_type="genomic DNA"
/sub_species="troglodytes"
/db_xref="taxon:37011"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%;
76.9%;
                                                                                                                                                                                                            Tanaka, Y., Yoshida, T. and Watanabe, K.
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Pred. No. 2.4e
3; Mismatches
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ORGANISM
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KPN344089
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KATSUMI WATANABE
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/02,
C12N15/00,C12N5/00
CC CC Location/Qualifiers
PH Key 1 .1197
FT source /organism='Hyphomicrobium sp.'.
                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-JUL-2002) Domenech-Sanchez A., Biologia, Area de Submitted (15-JUL-2002) Domenech-Sanchez A., Biologia, Area de Microbiologia, Universitat de les Illes Balears and IMEDEA (CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (09-AUG-2001) Domenech-Sanchez A., Biologia, Area de Microbiologia, Universitat de les Illes Balears and IMEDEA (CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca, 07071, SPAIN
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Klebsiella pneumoniae
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Klebsiella pneumoniae ompK36
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3 (bases 1 to 1241)
Domenech-Sanchez, A.
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                                                                                                                                                                                                                                                                 , 2002 this sequence version replaced gi:15149830
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:82"
/product="OmpK36 protein"
                   /codon_start=1
/transl_table=11
                                                        /gene="ompK36"
/function="porin"
                                                                                              117. .1235
                                                                                                            /gene="ompK36"
                                                                                                                                                                                                          organism="Klebsiella pneumoniae"
|mol_type="genomic DNA"
                                                                                                                                                     country="United Kingdom"
                                                                                                                                                                        db_xref="taxon:573"
                                                                                                                                                                                          isoTate="103624"
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Pred. No. 2.4e+04;
3; Mismatches 0
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11525977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-FEB-2001) Soutourina O.A., moleculaire, Pasteur Institute, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacter sp. 22
Enterobacter sp. 22
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AJ308467.1 GI:15551737
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Enterobacteriaceae; Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soutourina, O.A., Semenova, E.A., Parfenova, V.V., Danchin, A. and
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/db_xref="G1:J5149831"
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/db_xref="InterPro:IPR003229"
/d
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180. .1232
                                                                                                                                                                                                                                                                                                                                                 /organism="Enterobacter sp.
/mol type="genomic DNA"
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/product="mature OmpK36 protein'
/function="porin"
                                                                                                                                  /gene="168 rRNA"
/product="168 ribosomal RNA"
                                                                                                                                                                                                                                                                                                                     mol_type="genomic
isolate="22"
                                                                                                                                                                                                               gene="168 rRNA"
                                                                                                                                                                                                                                                                 country="Russia:Lake Baikal"
                                                                                                                                                                                                                                                                                               db_xref="taxon:151779"
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                      92.9%;
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Pasteur, 28, rue du Dr.
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AY985162
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Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A. Direct Submission
Submitted (28-MAR-2005) Division of Infectious Diseases & Geographic Medicine, Stanford University School of Medicine, 300 Geographic Pasteur Drive, Palo Alto, CA 94305, USA
Location/Qualifiers
                                                                  2 (bases 1 to 1356)

Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E.,

Sargent, M., Gill, S.R., Nelson, K.B. and Relman, D.A.

Direct Submission
                                                                                                                                                         1 (bases 1 to 1356)
Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E.,
Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A.
Diversity of the human intestinal microbial flora
                                                                                                                                                                                                                                                  uncultured bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GUACUGCAACUCG 14
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Pasteur Drive, Palo Alto, CA 94305, USA
Location/Qualifiers
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isolation_source="from human stool sample"
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Eckburg, P.B., Bik, E.M., Bernstein, C.N., Purdom, E., Sargent, M., Gill, S.R., Nelson, K.E. and Relman, D.A. Diversity of the human intestinal microbial flora
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969 11.8 65.6 930 12 US-11-165-160-1 Sequence.	11 8 65 6 66 10 IIS-11-110-880-7 Sequence	11.8 65.6 867 8 US-10-750-185-3/322 sequence 3/322,	11.8 65.6 844 9 US-11-096-568A-1723	11.8 65.6 832 6 US-09-925-065A-555069 Sequence 555069	963 11.8 65.6 820 12 US-11-136-527-3181 Sequence	962 11.8 65.6 775 6 US-09-925-065A-939412 Sequence 939412,	961 11.8 65.6 775 6 US-09-925-065A-85135 Sequence 85135,	960 11.8 65.6 742 6 US-09-925-065A-26766 Sequence 26766,	959 11.8 65.6 742 6 US-09-925-065A-26765 Sequence	958 11.8 65.6 742 6 US-09-925-065A-26764 Sequence 26764,	957 11.8 65.6 739 6 US-09-925-065A-9189 Sequence 9189,	11.8 65.6 736 6 US-09-925-065A-92394 Sequence 92394,	11.8 65.6 724 6 US-09-925-065A-17137 Sequence 17137,	11.8 65.6 724 6 US-09-925-065A-1/136 Sequence 1/136	11. 11. 0 17	10 053 11 0 05 0 720 0 10-10-10-13286 Commonto 15286	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	951 11 8 65 6 717 6 US-09-925-065A-84761 Sequence 84761.	11.8 65.6 706 6 US-09-925-065A-735325 Sequence 735325	949 11.8 65.6 684 12 US-11-055-822-773 Sequence	948 11.8 65.6 683 6 US-09-925-065A-709227 Sequence 7092	947 11.8 65.6 679 6 US-09-925-065A-867507 Sequence	946 II.8 65.6 6// 6 US-09-925-065A-925316 Sequence	TO OUT O TO OUT O TO OUT OUT OUT OUT OUT	945 11 8 65 6 664 6 US-09-925-065A-954431 Sequence	944 11.8 65.6 661 6 US-09-925-065A-921939 Sequence	11.8 65.6 658 6 US-09-925-065A-955285 Sequence	11.8 65.6 65.6 08-09-931236 sequence	042 11 8 65 6 658 6 IIS-09-925-0658-931238 Semience	941 11.8 65.6 653 6 US-09-925-065A-926677 Sequence 9	940 11.8 65.6 650 6 US-09-925-065A-56116 Sequence 5	AND THE COLOR OF COLOR OF THE TAIL CONTRACTOR OF THE COLOR OF THE COLO	020 11 8 65 6 650 6 TS-00-035-0658-56115 Semience 5	11 8 65 6 645 12 US-11-234-786-635 Semience	11.8 65.6 645 9 US-11-096-568A-947 Sequence 9	936 11.8 65.6 640 6 US-09-925-065A-460290 Sequence	935 II.8 65.6 640 6 05-09-25-005A-460269 Sequence 4	DOES 11 0 CE C CAN C TO COURTER AND COMMON OF A	934 11 8 65 6 634 6 IIS-09-925-065A-124541 Semience 1	933 11.8 65.6 629 6 US-09-925-065A-460288 Sequence 4	932 11.8 65.6 629 6 US-09-925-065A-125262 Sequence 1	931 11.8 65.6 629 6 US-09-925-US5M-125261 Sequence 1	11 0 CE C COO C TO 00 00 00 00 00 00 00 00 00 00 00 00 00	930 11.8 65.6 628 6 US-09-925-065A-938606 Sequence 9	11.8 65.6 627 6 US-09-925-065A-804149 Sequence 8	11.8 65.6 624 6 US-US-925-065A-746796 Sequence 7	THE COURSE OF THE CONTRACT OF	11 8 65 6 633 6 IIC-09-935-0653-745513 Semience 7	926 11.8 65.6 619 6 US-09-925-065A-847077 Sequence 8	925 11.8 65.6 618 6 US-09-925-065A-675663 Sequence 6	924 11.8 65.6 617 6 US-09-925-065A-82069/ Sequence 8	11.8 65.6 614 12 US-11-136-52/-3433 Sequence	11.0 00.0 01# 0 00-940-000M-709407 Degreeted 7	DOOD 11 0 NE N NIL NIL NIL NIL NIL NIL NIL NIL NIL N	021 11 8 65 6 613 6 IIS-09-925-0658-852305 Segments	920 11.8 65.6 613 6 US-09-925-065A-472687 Sequence	11.8 65.6 612 6 US-09-925-065A-533309 Sequence	11.8 65.6 611 6 US-09-925-065A-851832 Sequence 851832	11.8 65.6 60 05-04-342000 05-04-342000 05-04-342000 05-04-342000	THE OUT OF THE PROPERTY AND THE PROPERTY	11 0 6E 6 60E 6 TIS-00-03E-06EN-307EA1 Seminare	11 8 65 6 604 6 US-09-925-065A-858157 Sequence 85815	11.8 65.6 600 12 US-11-128-049-4077 Sequence 4077	11.8 65.6 600 12 US-11-128-061-4077 Sequence 4077	912 11.8 65.6 600 12 US-11-136-527-8178 sequence 8178	11.8 65.6 600 12 US-11-136-52/-/529 Sequence /529	11.8 65.6 600 12 US-11-136-52/-6336 Sequence	11.8 65.6 600 8 US-10-/50-623-2846 Sequence 2040,	11.0 00.0 00.0 0.00 0.00 0.00 0.00 0.00	11 0 CE C COO 0 TG-10-750-105-2049 Comience 2848	907 11.8 65.6 600 6 US-09-925-065A-489928 Sequence	906 11.8 65.6 599 6 US-09-925-065A-836235 Sequence	905 11.8 65.6 599 6 US-09-925-065A-836234 Sequence 836234	11.8 65.6 598 8 US-10-750-623-4223 Sequence 4223,	11.8 65.6 598 8 05-10-120-4223 Sequence	11.0 00.0 070 0 100 100 100 100 000 000 000 000	000 11 0 65 6 506 6 HS-00-005-0653-843350 Semionre	901 11.8 65.6 596 6 US-09-925-065A-815733 Sequence 815733	11.8 65.6 596 6 US-09-925-065A-277336 Sequence	899 11.8 65.6 596 6 US-09-925-065A-277335 Sequence	898 11.8 65.6 593 6 US-09-925-065A-382019 Sequence	897 11.8 65.6 591 6 US-09-925-065A-779314 Sequence	007 11 0 CE C E01 C TO 00.035-0667-77011A Comiente

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PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILING DATE: 1997-10-30
PRIOR PILING DATE: 1996-10-30
PRIOR PILING DATE: 1996-10-30
PRIOR PILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-02-07
PRIOR PILING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
PRIOR DATE: 1995-02-07
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                                                                                                           ; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-279-60
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                                                                                                                                                                                                                                                                                                               Sequence 60, Application US/10619279
Publication No. US20050267057A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
FILE REFERENCE: C1039/7023/HCL
CURRENT APPLICATION NUMBER: US/10/619,279
CURRENT FILING DATE: 2003-07-14
CURRENT FILING DATE: 2003-07-14
                                                            Query Match
Best Local Similarity
Matches 16; Conser
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                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                          AGAGGGUCGCACGCGGUA 18
               AGAGGGTCGCACGCGGTA 1
                                                              Conservative
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US-10-91-696-568A-18135
US-09-925-065A-40401
US-09-925-065A-3148
US-10-932-182A-3148
US-10-932-182A-37956
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US-09-925-065A-16872
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US-10-932-182A-7635
US-09-925-065A-13519
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US-09-925-065A-713519
US-09-925-065A-713519
US-09-925-065A-713519
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US-11-245-147-81
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US-11-128-049-3370
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                                                              Mismatches
                                                                                  BB
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                                                                                   Length 18;
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Sequence 40402, A
Sequence 3148, Ap
Sequence 3148, Ap
Sequence 37956, A
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Sequence 18135, A
Sequence 40400, A
Sequence 40401, A
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Sequence
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Sequence 24, Appl
Sequence 7, Appli
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CURRENT APPLICATION NUMBER: US/10/497,591A
CURRENT FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: PCT/EP02/13791
PRIOR FILING DATE: 2002-12-05
PRIOR APPLICATION NUMBER: A 1924/2001
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 113
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 41
LENGTH: 18
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US-10-497-591A-41/c
; Sequence 41, Application US/10497591A
; Publication No. US20050250716A1
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; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-11-127-654-4
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US-11-127-654-4/c
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Matches 16
Query Match
Best Local S
Matches 13
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APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
CURRENT APPLICATION NUMBER: US/11/127,654
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/112,653
PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
NUMBER OF ERQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
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Publication No. US20050250726A1
GENERAL INFORMATION:
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                                                                             NAME/KEY: modified base LOCATION: (5)..(11)
OTHER INFORMATION: n = inosine or uracil
-10-497-591A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHMIDT, WALTER
APPLICANT: SCHELLACK, CAROLA
APPLICANT: EGYED, ALENA
APPLICANT: LINGNAU, KAREN
TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGODEOXYNUCLEOTIDES
FILE REFERENCE: SONN:045US
                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE: THEORY OTHER INFORMATION: Description OTHER INFORMATION: Primer
                                                                                                                                                            FEATURE:
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13; Conserv
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83.3%;
llarity 72.2%;
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2; Mismatches
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Pred. No. 1
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SEQ ID NO 990315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/310,914A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LU, Yu-Ping et al.
TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1581PUS2
CURRENT APPLICATION NUMBER: US/10/981,334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 21, Application US/10981334 iblication No. US20060008816A1
                                                                       PPLICANT: CIBELLI, JOSE
                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 935
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                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                              864 AGGGTCGCACGCGGT 878
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                                                                                                                                                                                                                                              3 AGGGUCGCACGCGU 17
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FERNANDEZ, EMILIO O.
JORDAO DE MEGALHAES, GUILHERME
KOCABAS, ARIF
CROSBY, JAVIER A.
                                                                                                         Application US/11091883 o. US20060024693A1
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                   Promoter and/or promoter control element identified from Arabidopsis thaliana or Oryza sativa.
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Pred. No.
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                                                                                                                      SOFTWARE: Pater
SEQ ID NO 55765
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 55765, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                        CURRENT PILICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 513
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CURRENT FILING DATE: 2005-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
                                                                                                                                                           NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                               APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MMI GENOMICS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-750-185-55765
                                                                    TYPE: DNA
ORGANISM: Bovine
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OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WAME/KEY: modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: a, c,
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LOCATION: (909)..(909)
                                                                                                     ENGTH: 2106
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                                                                    19866881108267
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 82.2%;
77.8%;
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 Score 14.8;
Pred. No. 6
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; ORGANISM: Bovine 
US-10-750-185-37497
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APPLICANT: DMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: HORENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
                                                                                                                                                                                                                                          FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 37497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INPERRING BOVINE TRAITS

FILE REFERENCE: MMILIO-1

CURRENT APPLICATION NUMBER: US/10/750,623

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION OF SEQ 10 NOS: 64922

SOFTWARE: Patentin version 3.1

SEQ 1D NO 55765
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37497, Application US/10750185 Publication No. US20050260603A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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ORGANISM: Bovine
                                                                                                                                                                                                     TYPE: DNA
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                AGAGGGUCGCACGCGG 16
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KERR, Richard
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77.8%;
                                                         80.0%; Score 14.4; DB 8;
93.8%; Pred. No. 1.1e+02;
tive 0; Mismatches 1;
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APPLICANT: MOI GENOMICS, SUE K.

APPLICANT: LOENISE, SUE K.

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: BATES, Stephen

APPLICANT: MOINTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMII100-1

CURRENT APPLICATION NUMBER: US/10/750,623

CURRENT APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR APPLICATION STEPHENCE: US 60/437,482

PRIOR APPLICANT: US 60/437,482
RESULT 12
US-10-750-185-4096/c
; Sequence 4096, Application US/10750185
; Publication No. US20050260603A1
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; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-37497
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; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-531952
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Sequence 531952, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
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US-10-750-623-37497/c
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SEQ ID NO 531952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded St
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 673904
                                                                                                                                                                                                                                                                    Local
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US-09-925-065A-552179/c
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; ORGANISM: Bovine MMBT19288
US-10-750-185-4096
                                                                                                                                                                                                                                                                                                                                         CRGANISM: Bovine MMBT19288
JS-10-750-623-4096
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Best Local Similarity 87.5
14; Conservative
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SEQ ID NO 4096
LENGTH: 600
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NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 4996
LENGTH: 600
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                                                        Sequence 552179, Application US/09925065A Publication No. US20040181048A1
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CURRENT EILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIllOO-1
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Local Similarity 87.5%;
es 14; Conservative
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ion No. US20050287531A1
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KERR, Richard
ROSENFELD, David
HOLM, Tom
BATES, Stephen
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Identification and Mapping of Single
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87.5%;
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Pred. No.
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Pred. No.
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; TYPE: DNA; Homo sapiens US-09-925-065A-649799
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Best Local Similarity 92.9%;
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                                                                                                                                       Query Match
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2000-10-24
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CURRENT FILING DATE: 2001-08-08
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  292
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                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                             PastSEQ for Windows Version 4.0
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GAGGGTGGCACGCAGTA 308
                                              GAGGGUCGCACGCGGUA 18
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                                                                                                               76.7%;
76.5%;
                                                                                           Score 13.8; DB 6; Length 414; Pred. No. 2.5e+02; 2; Mismatches 2; Indels
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Pred. No. 1
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Sequence 99074, Application US/09925065A Publication No. US20040181048A1

-09-925-065A-99074/c

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; ORGANISM: Homo sapiens
US-09-925-065A-99074
                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-925-065A-151643
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PRIOR PRIOR DATE: 2001-05-09
NUMBERD DATE: 2001-05-09
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-55-09
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                                                                                            Matches
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Best Local :
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-24
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/09/925,065A
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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118
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                                           AGAGGGUCGCACGCGGU 17
AGAGGGTCGAACGCCGT 134
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llarity 76.5%;
Conservative
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76.5%;
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Pred. No. 2.5e
2; Mismatches
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Pred. No. 2
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                                                                                                                                   6; Length 577;
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RESULT 18

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AGAGGGTCGAACGCCGT 134

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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-925-065A-151644
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151645
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151644
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                                                                   Query Match
Best Local S
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TITLE OF INVENTION: Identification and Mapping
TITLE OF INVENTION: Nucleotide Polymorphisms i
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 108827.135
                                                                                                                                                           LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
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    1 AGAGGGUCGCACGCGGU 17
                                                                     Similarity
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                                                Conservative
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76.5%;
                                                                     76.7%;
76.5%;
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                                              Score 13.8; DB 6;
Pred. No. 2.5e+02;
2; Mismatches 2;
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Pred. No. 2.5e+02;
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in the Human
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                                                                                                                     Query Match
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-09-925-065A-709998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1592PUS2
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TITLE OF INVENTION: Sequence-Determine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
IITLE OF INVENTION: Identification and Mapping
IITLE OF INVENTION: Nucleotide Polymorphisms i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-11-30
APPLICATION NUMBER: US 60/261,766
FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/252,147
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451
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FILING DATE: 2005-04-0
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                                                                                                Similarity
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76.5%;
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Pred. No. 2.4e
2; Mismatches
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                                                                                                                     Length 1492;
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RESULT 22 US-10-240-708-20

AGAGGGUCGCACGCGGU 17

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; ORGANISM: Homo sapiens
US-09-925-065A-74944
                                                                                                                                                                     SEQ ID NO 74944
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CURRENT FILING DATE: 2002-10-03
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TITLE OF INVENTION: Diagnosis of Diseases
TITLE OF INVENTION: by Assessing DNA Meth
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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CURRENT FILING DATE: 2001-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-11-30
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blication No. US20040181048A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANY: Wang, David G.
TTLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/261,766
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Similarity
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76.5%; Pred. No. 2.3
tive 2; Mismatches
                                                                                                                                                                                            Version 4.0
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AGAGGGCCRGACGCGGT 289

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Sequence 299863, Application US/09925065A

| Publication No. US20040181048A1
| GENERAL INFORMATION: US20040181048A1
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
| CURRENT APPLICATION NUMBER: US/09/925,065A
| CURRENT FILING DATE: 2001-08-08
| PRIOR APPLICATION NUMBER: US 60/243,096
| PRIOR APPLICATION NUMBER: US 60/243,096
| PRIOR FILING DATE: 2000-11-24
| PRIOR FILING DATE: 2000-11-20
| PRIOR APPLICATION NUMBER: US 60/252,147
| PRIOR APPLICATION NUMBER: US 60/250,092
| PRIOR APPLICATION NUMBER: US 60/250,092
| PRIOR FILING DATE: 2000-11-30
                                                                             ; ORGANISM: Homo sapiens US-09-925-065A-299863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-46507
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US-09-925-065A-46507
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILLING DATE: 2001-01-05-09
PRIOR FILLING DATE: 2001-05-09
                                                                                                                                                     SOFTWARE: FastS
SEQ ID NO 299863
LENGTH: 589
Query Match
Best Local Similarity
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                TYPE: DNA
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  74.4%;
80.0%;
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Pred. No. 4.
Score 13.4; DB 6;
Pred. No. 4.2e+02;
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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1781
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47629
LENGTH: 605
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                                                                                                                                                                                                            SEQ ID NO 1781
LENGTH: 1185
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                                                                            Matches
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                       APPLICANT: Wyeth
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OP INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AMI.01086)
CURRENT APPLICATION NUMBER: US/11/136,527`
CURRENT FILING DATE: 2005-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/574,294 PRIOR FILING DATE: 2005-05-26
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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                                                                                              Match 74.4%;
Local Similarity 80.0%;
  907
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                                      3 AGGGUCGCACGCGGU 17
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AGGGTCGCACGCGTT 893
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                                                                            Conservative
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93.3%;
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Pred. No. 4.2e+02;
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                                                                                              Score 13.4; DB 12; Pred. No. 4.1e+02;
                                                                              Mismatches
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SEQ ID NO 62892
                                                                                 Matches
                                                                                                                         Query Match
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-10-750-185-62892
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                 ORGANISM: Bovine
10-750-623-62892
                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: MMII100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                             WIMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MMI GENOMICS, INC.
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ublication No. US20050287531A1
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blication No. US20050260603A1
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775
                                                                                                     Similarity
GGGTTGCACGCGGTA 761
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KERR, Richard
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                                                                                 Conservative
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80.0%; Pred. No. 4
                                                                                                 74.4%; Score 13.4;
80.0%; Pred. No. 4
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RESULT 30

l1-082-154A-118/c

blication No.

Application US/11082154A
o. US20060024820A1

Perkins, Edward

Perez,

Carl

Lindenbaum, Michael

Greene, Amy Leung, Josephine Fleming, Elena Stewart, Sandra

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US-10-912-971-1
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                                                                          Matches
                                                                                                               Query Match
                                                                                                                                                                                                                                    SEQ ID NO 1
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CURRENT FILING DATE: 2004-08-06
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APPLICANT: Yaver, Debbie
TITLE OF INVENTION: Polypeptides Having Alpha-Glucosidase Activity And
TITLE OF INVENTION: Polynucleotides Encoding Same
                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 18
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TYPE: DNA
ORGANISM: Aspergillus fumigatus
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                              ENGTH: 4663
                                                                                                 Local
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13; Conserv
                                                                                                 Similarity
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No. US20060029546A1
GGGTCGCACGCGGCA 1150
                                      GGGUCGCACGCGGUA 18
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                                                                            Conservative
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                                                                                             74.4%; Score 13.4;
86.7%; Pred. No. 4
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86.7%; Pred. No. 46
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US-11-082-154A-18/c
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SEQ ID NO 118
                                                                                                            Query Match
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Best Local (
                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X82564
DATABASE ENTRY DATE: 1996-04-09
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 10/161,403
PRIOR FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 17084-022003 (420C)
CURRENT APPLICATION NUMBER: US/11/082,154A
CURRENT FILING DATE: 2005-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Mic
APPLICANT: Greene, Amy
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PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 10/161,403
PRIOR FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fleming, Blena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
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CURRENT FILING DATE: 2005-03-15
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                            ENGTH: 22118
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                                                                                           Local
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7580
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                                                                                         Similarity
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                                    AGAGGGUCGCACGCG 15
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Leung, Josephine
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Lindenbaum, Michael
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                                                                   74.4%; Score 13.4; Ilarity 93.3%; Pred. No. 3.8c Conservative 0; Mismatches
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                                                                                         .8e+02
                                                                                                        DB 12;
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                                                                     Gaps
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RESULT 34

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; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-355753
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US-11-121-849-355753
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US-10-933-982-106785
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                                                                                                                                                                                                                                                                                                                                         RESULT 36
                                                                                                                GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hums
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/933,982
CURRENT FILING DATE: 2004-09-03
NUMBER OF SEQ ID NOS: 224976
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 106785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Barts, Jennifer
TITLE OF INVENTION: Methods
FILE REFERENCE: 3700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355753, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 290316, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 355753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 106785, Application US/10933982
Publication No. US20060051769A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded
TITLE OF INVENTION: Microarrays
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
NUMBER OF SEQ ID NOS: 673904
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
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72.2%;
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77.8%;
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Pred. No. 5.8e
1; Mismatches
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Pred. No. 5.8e+02;
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JS-09-925-065A-143833
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JS-09-925-065A-354563
                                                                                                                                                                                                                 Sequence 143833, Application US/09925065A Publication No. US20040181048A1
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                                                                                                                  ENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                 CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR FILING DATE: 2001-01-16
                                                                                                         FILE REFERENCE: 108827.135
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ITLE OF INVENTION: Identification and Mapping of Singl
ITLE OF INVENTION: Nucleotide Polymorphisms in the H
                                          RIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                            2001-08-08
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US 60/252,147
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Pred. No. 5
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Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 514;
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GENERAL INFORMATION:

Dumas Milne Edwards, Jean-Baptiste

Severin

Full-length human cDNAs encoding potentially secreted proteins

quence 758, Application US/10475075 blication No. US20060053498A1

-10-475-075-758

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; ORGANISM: Homo sapiens
US-09-925-065A-143833
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                                                                                                                  Query Match
                                                                                                                                                                                                                                           SEQ ID NO 143834
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CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/243,096
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                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                               OFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICANT: Wang, David G.
ITLE OF INVENTION: Identification and Mapping of Single
ITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE REFERENCE:
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APPLICATION NUMBER: US 60/289,846
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                                                                                                 Similarity
                                      AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                     [CATION NUMBER: US 60/261,766
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77.8%;
                                                                                               73.3%;
                                                                            pred. No. 5.4e
1; Mismatches
                                                                                               4e+02
                                                                                                                    Length 526;
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FILE REFERENCE: G-081USUSFL:
CURRENT APPLICATION NUMBER: US/10/475,075
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/IB01/00914
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 918
SOFTWARE: Patent.pm
SEQ ID NO 758
LENGTH: 543
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US-09-925-065A-742789
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US-09-925-065A-742789/c
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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Best Local S
Matches 13
                                                                                                                                                                                 Sequence 505693, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 742789, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.1.35
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 548
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Similarity 77.8%;
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Pred. No. 5.4e+02;
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Pred. No. 5
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US-09-925-065A-847993/c
; Sequence 847993, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-839454
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; Sequence 839454, Application US/09925065A
; Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-505693
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                                                                                                                                                                                               RESULT 44
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 839454
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR EPILICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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PRIOR FLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 584
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Local Similarity 72.2%;
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PILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
APPLICATION NUMBER: US 60/261,766
FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                         13; Conservative
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                                                                                                                                                                                                                                                            AGAGGGTCTCACTTGGTA
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                                                                                                                                                                                                                                                                                                                                                                  73.3%;
72.2%;
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Pred. No. 5.4e+02;
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Pred. No. 5.4e+02;
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RESULT 46
US-09-925-065A-516743
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US-09-925-065A-516742
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US-09-925-065A-847993
                                                     Sequence 516743
Publication No.
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                                      GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
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CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/252,147 FILING DATE: 2000-11-20
                                                                                                                                                                                      429 AGAGGGTGGCACCCTGTA 446
                                                            516743, Application US/09925065A
ion No. US20040181048A1
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Identification and Mapping of Single
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Pred. No. 5
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                            6; Length 594;
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; ORGANISM: Homo sapiens
US-09-925-065A-516743
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LENGTH: 594
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                                                                                    Matches
                                                                                                                             Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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PRIOR FILING DATE: 2000-10-24
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CURRENT FILING DATE: 2001-08-08
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PRIOR APPLICATION NUMBER: US 60/252,147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/289,846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
                                                                                    13;
                                                                                                           Similarity
AGAGGGTGGCACCCTGTA
                                         AGAGGGUCGCACGCGGUA 18
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                                                                                    Conservative
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                                                                                                         73.3%;
72.2%;
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  446
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                                                                                  Score 13.2; I
Pred. No. 5.46
2; Mismatches
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Pred. No. 5
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                                                                                                                               Length 594;
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US-09-925-065A-151923 ; Sequence 151923, Application US/09925065A ; Publication No. US20040181048A1

RESULT 48

GENERAL INFORMATION:

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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
                                                                                                                                                                                                                    ; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-841497
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US-09-925-065A-841497
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; ORGANISM: Homo sapiens
US-09-925-065A-151923
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 841497
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                              Query Match
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                                                                                                           Matches
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
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PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 603
                                                                                                                                     Local
457
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                                                                                                                                     Similarity
                                                AGAGGGUCGCACGCGGUA 18
AGAGGGTGGCAGGAGGTA 474
                                                                                                     73.3%; Score 13.2; DB 6; Length 625; llarity 72.2%; Pred. No. 5.4e+02; Conservative 2; Mismatches 3; Indels
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RESULT 50

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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
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PRIOR PILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 821405
LENGTH: 629
TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-821405
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Search completed: March 19, 2006, 05:42:21 Job time: 1217.62 secs
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Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/925,065A
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	971 12.8 71.1 990 7 US-10-767- 972 12.8 71.1 996 7 US-10-437-	970 12.8 71.1 971 9 US-10-363-483A-283	968 12.8 71.1 971 8 US-10-363-345A-283 969 12.8 71.1 971 9 US-10-363-483A-283	12.8 71.1 971 8 US-10-363-345A-283	965 12.8 71.1 970 6 US-10-330-U518 966 12.8 71.1 970 7 US-10-437-963-	964 12.8 71.1 967 9 US-10-363-483A	963 12.8 71.1 967 9 US-10-363-	961 12.8 71.1 967 8 US-10-363-3458	960 12.8 71.1 957 6 US-10-156-761-	12.8 71.1 955 8 US-10-425-115-	958 12.8 71.1 954 7 US-10-424-599-	956 12.6 /1.1 953 B US-10-620-246-	12.6 /1.1 952 3 US-U9-804-	12.8 71.1 952 3 US-09-791-	953 12.8 71.1 939 7 US-10-437-963-839	952 12.8 71.1 933 7 US-10-767-701-9241	951 12.8 71.1 925 7 US-10	949 12.8 /1.1 900 8 US-10	12.8 71.1 896 7 US-10	47 12.8 71.1 886 8 US-10	46 12.8 71.1 881 8 US-10	45 12.8 71.1 881 7 US-10	944 12.8 71.1 879 7 US-10	943 12.8 71.1 867 3 US-09	942 12.8 71.1 858 9 US-10	941 12.8 71.1 845 9 US-10	040 128 71 1 845 1 1040	938 12.8 71.1 845 8 US-10	937 12.8 71.1 839 7 US-10	12.8 71.1 838 4 US-09	935 12.8 71.1 807 7 US-10-437-963-64782	934 12.8 71.1 805 4 US-09	933 12.8 71.1 801 6 US-10	931 12.8 /1.1 /96 / US-10	930 12.8 71.1 790 8 US-10-425-115-4	929 12.8 71.1 787 8 US-10-425-115-1	12.8 71.1 786 6 US-10-313-542-2	927 12.8 71.1 785 6 US-10-414-080-1	926 12.8 71.1 785 3 US-09-853-386-6	925 12.8 71.1 784 9 US-10-363-483A-	924 12.8 71.1 784 9 US-10-363-483A-	923 12.8 71.1 784 8 US-10-363-345A	12.8 71.1 784 8 US-10-363-345A	12.6 /1.1 //1 0 03-10	12 8 71 1 771 6 IN-10-369-493-4	010 13 0 71 1 764 0 US-10-684-422-4	917 12.8 71.1 762 7 US-10	12.8 71.1 757 6 US-10	915 12.8 71.1 757 5 US-10	914 12.8 /1.1 /51 9 05-10	912 12.8 /1.1 /51 9 US-10	911 12.8 71.1 751 8 US-1	910 12.8 71.1 751 8 US-10	909 12.8 71.1 734 9 US-10	908 12.8 71.1 734 9 US-10	907 12.8 71.1 734 8 US-10	905 12.8 71.1 714 8 [15-10	904 12.8 /1.1 /1/ 4 US-09	903 12.8 71.1 716 8 US-10-425-115-7897	902 12.8 71.1 705 7 US-10	12.8 71.1 702 7 US-10	00 12:8 71.1 701 6 US-10
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APPLICANT: Weiner, George

TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines

FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/824,468
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/286,098
PRIOR FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPES: DNA
COCANITGM. Aprificial Semigence
                   RESULT 2
US-09-888-326-485/c
US-09-888-326-485, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
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APPLICANT:
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Local Similarity 88.9%;
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US-10-10-117-722-734
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US-10-10-28-61-734
US-10-10-28-61-734
US-10-10-28-1-633
US-10-10-28-1-13828
US-10-156-761-4351
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Matches
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RESULT 4

US-09-776-479-56/c

; Sequence 56, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: FOURON, Yves
; TITLE OF INVENTION: Immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Petersen, Deanna M.

APPLICANT: Pouron, Yves

TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy

FILE REFERENCE: C1037/7013 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/09/776,479

CURRENT APPLICATION NUMBER: US 60/179,991

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR APPLICATION NUMBER: US 60/179,991

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 1093

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 18
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TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
TITLE REFERENCE: C1039/7052 (AWS)
CURRENT ELIZATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOPTWARE: PASTESEQ for Windows Version 3.0
SEQ ID NO 485
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: phosphorothicate backbone
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PEATURE:
OTHER INFORMATION: Synthetic Sequence
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Pred. No. 13;
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Immunostimulatory Nucleic Acids for the

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URRENT APPLICATION NUMBER: US/09/776,479
URRENT FILING DATE: 2001-02-02

Treatment of Asthma and Allergy

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RESULT 6
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PRIOR FILING DATE: 2000-02-03
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URRENT APPLICATION NUMBER: US/09/954,987B
URRENT FILING DATE: 2001-09-17
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PPLICANT: Hermann Wagner
TILE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
ITLE OF INVENTION: CPG-BASED IMMUNO-AGONIST/ANTAGONIST
                                                                                                                                                                                                                                                                                                  EATURE:
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Application
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No. US20030104523A1
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  US/09776479
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GENERAL INFORMATION:

4, Application US/10112653 on No. US20030050268A1

APPLICANT: Krieg, Arthur M. APPLICANT: Berg, Daniel J.

C01039/70060 (AWS)

INFLAMMATORY DISEASES

10-112-653-4/c

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; OTHER INFORMATION: Synthetic Sequence US-09-776-479-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-776-479-56/c
                                                                                                                                                                              SEQ ID NO 56
LENGTH: 18
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/776,479
                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1093
                                                                                                                                                                                                                                                                                                                                                                                                               MERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                PPLICANT:
                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                             OTHER INFORMATION: Synthetic Sequence
                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                              PPLICANT: FOURON, Yves
(TLE OF INVENTION: Immunostimulatory Nucleic Acids for TILE OF INVENTION: Treatment of Asthma and Allergy (LE REFERENCE: C1037/7013 (HCL/MAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                16;
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                                               Similarity
                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
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AGAGGGUCGCACGCGGUA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09776479
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                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                               Deanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%
                                              88.9%;
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                              2;
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                                                 Pred. No.
                                                               Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
                              Mismatches
                                                                DB 3;
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GENERAL INFORMATION:

APPLICANT: Bratzler, Robert L.

TITLE OF INVENTION: Inhibition of Angiogenesis by FILE REFERENCE: C1037/7025 (HCL/MAT)

CURRENT APPLICATION NUMBER: US/10/017,995

CURRENT FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: US 60/255,534

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 56

LENGTH: 18
                                                                                                                                                                                                                                                                                                                     US-10-017-995-56/c ; Sequence 56, Application US/10017995 ; Publication No. US20030055014A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bratzler, Robert L.
TITLE OF INVENTION: Inhibition of Angiogenesis by
FILE REPERENCE: C1037/7025 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/255,534
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-017-995-4/c
US-10-017-995-56
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Sequence US-10-017-995-4
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Publication No. US20030055014A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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LENGTH: 18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: FastSEQ for Windows
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TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                   ORGANISM: Artificial Sequence FEATURE:
             OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
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                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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88.9%; Pred. No. 13;
tive 2; Mismatches
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Pred. No. 13
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                                                                                                                                                                                                                                                              by Nucleic Acids
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APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Methods for Treating and
TITLE OF INVENTION: Infectious Disease
FILE REFERENCE: CO1039.70062.US
CURRENT APPLICATION NUMBER: US/10/187,264A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-10-30
PRIOR FILING DATE: 1995-02-07
PRIOR FILING DATE: 1995-02-07
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US-10-187-264A-60/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-161-229-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/191,170
PRIOR FILLING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR FILLING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILLING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR FILLING DATE: 1995-02-07
PRIOR APPLICATION NUMBER: US 08/376,358
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILLING DATE: 1994-07-15
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/10187264A
Publication No. US20030162734A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 99
SOFTWARE: PatentIn version 3.1
SEQ ID NO 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Hartmann, Gunth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/161,229
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
TITLE OF INVENTION: Activating Dendritic Cells
FILE REFERENCE: C01039/70061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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APPLICATION NUMBER: US 08/276,358 FILING DATE: 1994-07-15
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88.9%; Pred. No. 13;
tive 2; Mismatches
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Pred. No. 13;
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; COTHER INFORMATION: Synthetic oligonucleotide US-10-265-072-75
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/265,072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lipford, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                 NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                  APPLICATION NUMBER: US 08/960,774 FILING DATE: 1997-10-30
                                                                                                                       APPLICATION NUMBER: US 09/630,319 FILING DATE: 2000-07-31
                                           FILING DATE: 1997-10-30
APPLICATION NUMBER: US 08/738,652
APPLICATION 1996-10-30
                                  APPLICATION NUMBER: US 08/386,063
                                                                                                                                                                          APPLICATION NUMBER: US/10/306,522
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                                                                                                                                                                                                         F: Steinberg, Alfred D. INVENTION: Methods for INVENTION: Infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                               Application US/10306522
vo. US20030191079A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US20030166001A1
ON NUMBER: US 08/276,358
                                                                                                                                                                                                                                                                                Arthur M
                  1995-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOLL-LIKE RECEPTOR 3 SIGNALING AGONISTS AND ANTAGONISTS
                                                                                                                                                                                                           Infectious Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; bru-
                                                                                                                                                         2002-11-27
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                                                                                                                                                                                                                         for Treating and Preventing
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US-10-306-522-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-0: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Immunostimulatory Nucleic Acids FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
                                                                                                                    CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
                                                                                                                                                                                                                                                                               equence 56, Application US/10314578 ublication No. US20030212026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-09-25
                                                                                                     PRIOR APPLICATION NUMBER: US 60/156,113
                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/156,113
                                                                                                                                                                                                                                                                                                                          .0-314-578-56/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                      PLICANT: Schetter, Christian
PLICANT: Vollmer, Jorg
TLB OF INVENTION: Immunostimulatory Nucleic Acids
LB REFERENCE: C1039/7035 (HCL/MAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/156,135
                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
ICATION NUMBER: US 60/227,436
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                                          1999-09-27
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                                                             US 60/156,135
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Pred. No. 13
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Sequence 60, Application US/10719493

Publication No. US20040087538A1

GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: Methods of Treating Cancer Using
TITLE OF INVENTION: Immunostimulatory Oligonuclectides
FILE REFERENCE: C1039/7021/HCL
CURRENT APPLICATION NUMBER: US/10/719,493

CURRENT APPLICATION NUMBER: US 08/960,774

PRIOR APPLICATION NUMBER: US 08/960,774

PRIOR PILING DATE: 1997-10-30

PRIOR PILING DATE: 1996-10-30

PRIOR PILING DATE: 1996-10-30

PRIOR PILING DATE: 1996-02-07

PRIOR PILING DATE: 1996-02-07

PRIOR APPLICATION NUMBER: US 08/386,063

PRIOR PILING DATE: 1995-02-07

PRIOR PILING DATE: 1995-02-07
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APPLICANT: Lipford, Grayson
ITILE OF INVENTION: Methods for Regulating Hematopoiesis
ITILE OF INVENTION: Wethods for Regulating Hematopoiesis
ITILE OF INVENTION: USing CpG-Oligonucleotides
FILE REFERENCE: CO1041,70035.US
CURRENT APPLICATION NUMBER: US/10/373,381
CURRENT ETLING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 09/241,653
PRIOR APPLICATION NUMBER: US 60/085,516
PRIOR APPLICATION NUMBER: US 60/085,516
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 90
SOSTWARE: FastSEQ for Windows Version 3.0
SOSTWARE: FastSEQ for Windows Version 3.0
LENGTH: 18
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US-10-719-493-60/c
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US-10-373-381-47/c
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SEQ ID NO 56
LENGTH: 18
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PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
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Local Similarity 88.9%; Pred. No. 1
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Similarity 88.9%;
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US-10-877-369-47/c

Sequence 47, Application US/10877369
Publication No. US20040234512A1
GENERAL INFORMATION:

APPLICANT: Wagner, Hermann APPLICANT: Lipford, Grays

APPLICANT: Lipford, Grayson
TITLE OF INVENTION: Methods for Regulating Hematopoiesis
TITLE OF INVENTION: Using CpG-Oligonucleotides
FILE REFERENCE: C1041.70002US01
CURRENT APPLICATION NUMBER: US/10/877,369
CURRENT FILING DATE: 2004-06-25

PRIOR APPLICATION NUMBER: US 09/241,653

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; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-627-331-60
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PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
PRIOR PELING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 08/960,774
PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1997-10-30
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR APPLICATION NUMBER: US 08/276,358
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                                                                 Matches
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                               SEQ ID NO 60
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Best Local Similarity
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CURRENT FILING DATE: 2003-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods for Treating and TITLE OF INVENTION: Infectious Disease FILE REFERENCE: C01039.70062.US
                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic Oligonucleotide
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18
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                  1 AGAGGGUCGCACGCGGUA 18
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AGAGGGTCGCACGCGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10627331
40. US20040106568A1
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                                                                 Conservative
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JS-10-831-778-4/c
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JS-10-877-369-47
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Best Local Similarity
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FILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/831,778
CURRENT FILING DATE: 2004-04-73
PRIOR TOTAL
                                                                                                                                                                                                                                                             10-831-778-56/c
equence 56, Application US/10831778
ublication No. US20040235774A1
                                                                                        APPLICANT: Petersen, Deanna M.
APPLICANT: Pouron, Yves
TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
TITLE OF INVENTION: Treatment of Asthma and Allergy
FILS REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/831,778
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ablication No. US20040235774A1
                                                            RIOR APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic Sequence
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                                                                                                                                                                                                                                                  VERAL INFORMATION
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                                                          CATION NUMBER: US 60/179,991
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ndows Version 3.0
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EQ ID NO 47

OFTWARE:

FastSEQ for Windows Version 3.0

PRIOR APPLICATION NUMBER: US 60/085,516

09/241,653

1999-02-02 TUMBER: US 1998-05-14

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Best Local Similarity
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Best Local Similarity
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FILE REFERENCE: C1041.70002US02
CURRENT APPLICATION NUMBER: US/10/876,965
CURRENT FILING DATE: 2004-06-25
                                                                                                                                          equence 47, Apublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/241,653 PRIOR FILING DATE: 1999-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods for Regulating Hematopoiesis
                                                    APPLICANT: Lipford, Grayson
IITLE OF INVENTION: Methods for Regulating Hematopoiesis
IITLE OF INVENTION: Using CpG-Oligonucleotides
                                                                                                                                                                                10-876-965-47/c
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                             INFORMATION:
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No. US20040235778A1
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Pred. No. 13
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Sequence 60, Application US/10627413
Publication No. US20050101554A1
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Klinman, Dennis
APPLICANT: Steinberg, Alfred D.
APPLICANT: Steinberg, Alfred D.
TITLE OF INVENTION: Methods for Treating and Pre
TITLE OF INVENTION: Infectious Disease
FILE REFERENCE: C01039.70062.US
CURRENT APPLICATION NUMBER: US/10/627,413
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 09/630,319
PRIOR FILING DATE: 2000-07-31
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US-10-627-413-60/c
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Publication No. US20050032731A1
GENERAL INFORMATION:
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Best Local &
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SEQ ID NO 1
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Best Local Similarity
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PRIOR FILING DATE: 1995-08-18
PRIOR APPLICATION NUMBER: 08/376,175
PRIOR FILING DATE: 1995-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P01936US06
CURRENT APPLICATION NUMBER: US/10/800,926
CURRENT FILING DATE: 2004-03-15
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NUMBER OF SEQ ID NOS: 3
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PRIOR FILING DAYE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/193,653
PRIOR FILING DAYE: 1998-11-17
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR FILING DAYE: 1996-10-29
PRIOR FILING DAYE: 1996-10-29
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TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF
TITLE OF INVENTION: TO THE IMMINENCE OF MICROBIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18
TYPE: RNA
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OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: oligoribonucleotide
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APPLICATION NUMBER: US 08/960,774
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Pred. No. 13;
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PRIOR APPLICATION NUMBER: US 08/738,652
PRIOR FILING DATE: 1996-10-30
PRIOR PELICATION NUMBER: US 08/386,063
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR APPLICATION NUMBER: US 08/276,358
PRIOR FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 124
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Methods of Treating Allergic and TITLE OF INVENTION: Asthmatic Disorders Using Immunosti FILE REFERENCE: C1039/7020/HCL CURRENT APPLICATION NUMBER: US/10/921,086 CURRENT FILING DATE: 2004-08-17 PRIOR PELLING DATE: 1990-06-21 PRIOR FILING DATE: 1999-06-21 PRIOR PELLING DATE: 1999-10-30 PRIOR APPLICATION NUMBER: US 08/960,774 PRIOR FILING DATE: 1997-10-30 PRIOR APPLICATION NUMBER: US 08/738,652 PRIOR APPLICATION NUMBER: US 08/386,063 PRIOR FILING DATE: 1996-10-30 PRIOR APPLICATION NUMBER: US 08/386,063 PRIOR FILING DATE: 1995-02-07 PRIOR APPLICATION NUMBER: US 08/366,358 PRIOR FILING DATE: 1994-07-15 PRIOR APPLICATION NUMBER: US 08/276,358 PRIOR FILING DATE: 1994-07-15 PRIOR SEQ ID NOS: 123 PRIOR FILING DATE: 1994-07-15 PRIOR PRIOR PRIOR PRIOR DATE: 1994-07-15 PRIOR PRI
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Publication No. US2005010155
GRNERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Kline, Joel N.
                                                                                                                                 Matches
                                                                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
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TYPE: DNA
ORGANIEM: Artificial Sequence
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OTHER INFORMATION: Synthetic Oligonucleotide
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AGAGGGTCGCACGCGGTA
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No. US20050101557A1
                                                                                                                                 Conservative
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Pred. No.
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RESULT 28
US-11-084-777-67/c
; Sequence 67, Application US/11084777
; Publication No. US20050181422A1
; GENERAL INFORMATION:

APPLICANT: Stefan Bauer

B. Lipford

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                                                                                                Query Match
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                                                                                                                                                 OTHER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILE OF INVENTION: Methods of Redirecting an ITLE OF INVENTION: Response Using Immunostit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URRENT APPLICATION NUMBER: US/11/084,777
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                                                                                                                                                                   FEATURE:
                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/738,652 FILING DATE: 1996-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/300,210
                                                                                                                                                                                                                                                                                                     FILING DATE: 1995-02-07
APPLICATION NUMBER: US 08/276,358
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/960,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/954,987
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/386,063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/263,657 FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-06-22
APPLICATION NUMBER: US 60/291,726
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                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
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WG DATE: 2000-09-15
                                AGAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/11071836
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ON: Response Using Immunostimulatory Oligonucleotides
C1039/7022/HCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arthur M.
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                                                                                 Pred. No.
                                                                                                Score 18;
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                                                              Mismatches
                                                                                                DB 10;
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                                                                                                                                          US-10-053-645A-43
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                                                                                                       Query Match
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SEQ ID NO 43
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                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ANTISENSE OLIGOMERS, IFILE REFERENCE: 10412-022-999 CURRENT APPLICATION NUMBER: US/10/053,645A CURRENT FILING DATE: 2002-01-22
                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/263,244 PRIOR FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-053-645A-43
                                                                                                                                          FEATURE:
OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
OTHER INFORMATION: Oligionucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Krieg, Arthur M.
                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uence 43, Ap
lication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE: C1039/7026/HCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/286,098 FILING DATE: 1999-04-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/080,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I: Weiner, George
INVENTION: Methods and Products for Stimulating the
INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
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   AGAGGGTCGCACGCGGTA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10053645A
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                                                                                      88.9%;
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                                                                                                       100.0%;
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                                                                                    Pred
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                                                                                                       Score 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                   AND HYBRID OLIGOMERS THEREOF
                                                                                                       DB 6; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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RESULT 32 US-10-053-645A-9/c

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; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense; OTHER INFORMATION: Oligionucleotide
US-10-053-645A-9
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US-10-822-205-5/c
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                                                                                                                                              RESULT 34
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                                                            Sequence 9, Application US/10961458 Publication No. US20050170377A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 17
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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APPLICANT: ROBERT E. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
TITLE OF INVENTION: ANTIGENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
FILE REFERENCE: 10412-022-999
CURRENT APPLICATION NUMBER: US/10/053,645A
CURRENT FILING DATE: 2002-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYMERIC OLIGONUCLECTIDE PRODRUGS
FILE REFERENCE: 213.1152CIP
CURRENT APPLICATION NUMBER: US/10/822,205
CURRENT FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60/462,070
PRIOR FILING DATE: 2003-04-13
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/263,244
PRIOR FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
APPLICANT: Reed, John C.
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
FILE REFERENCE: 04040/1200990-US7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GREENWALD, RICHARD B.
APPLICANT: ZHAO, HONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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PRIOR FILLING DATE: 2004-10-07
PRIOR PELLICATION NUMBER: US 09/375,514
PRIOR FILLING DATE: 1999-08-17
PRIOR FILLING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILLING DATE: 1998-05-18
PRIOR FILLING DATE: 1998-06-05
PRIOR FILLING DATE: 1995-06-05
                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BISENHUT, MICHAEL
APPLICANT: MIER, WALTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09781980 Publication No. US20010029035A1
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ERITJA, RAMON
APPLICANT: HABERKORN, UWE
TITLE OF INVENTION: OLIGONUCLEOTIDE CONJUGATES
FILE REFERENCE: 2502498.991110
CURRENT APPLICATION NUMBER: US/09/781,980
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: DE 100 06 572
PRIOR FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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PRIOR FILLING DATE: 1988-12-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2004-10-07
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PRIOR FILING DATE: 1993-09-20
PRIOR APPLICATION NUMBER: US 07/840,716
PRIOR FILING DATE: 1992-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                    LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17
 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAGGGUCGCACGCGGUA 18
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                                  1 AGAGGGUCGCACGCGGUA 18
AGAGGGTCGCACACGGTA 1
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.4%;
                                                                                        91.1%;
83.3%;
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Pred. No.
                                                                                            Score 16.4;
Pred. No. 9:
                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
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                                                                                                            Length 20;
                                                                         Indels
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                                                                         Gaps
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RESULT 36
US-11-021-729-58/c
US-11-021-729-58/c
; Sequence 58, Application US/11021729
; Publication No. US20050203042A1
; GENERAL INFORMATION:

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                                                                                             US-09-965-116A-79/c
                                                                                                                    RESULT 37
                                                         Sequence 79, Application US/09965116A Patent No. US20020137714A1
                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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OTHER INFORMATION: modified LNA nucleotide
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OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Phosphorothicate linkage
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)..(16)
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: modified LNA nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 5-methyl cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/586,340 FILING DATE: 2004-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/558,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/532,844 FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER: DK PA 2004 01629
                                                                                                                                                                           16 GAGGGTCGCACGCGGT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THRUE, CHARLOTTE ALBAEK
INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF BCL-2
                                                                                                                                                                                                               2 GAGGGUCGCACGCGGU 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICATION NUMBER: US/11/021,729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATION NUMBER: DK PA 2004 00517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATION NUMBER: DK PA 2004 01069
                    Kandimalla, Ekambar R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WESTERGAARD,
Zhao, Qiuyan
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                                                                                                                                                                                                                                                                        Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                             DB 10;
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                                                                                                                                                                                                                                                                                           Length 16
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US-09-965-116A-80/c
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                                                                                                                                                                                                             SEQ ID NO 80
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PEATURE:
NAME/KEY: modified base
LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
-09-965-116A-80
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CURRENT APPLICATION NUMBER: US/09/965,116A
CURRENT FILING DATE: 2002-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 09/712,898
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                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/235,453
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/712,898
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PRIOR FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Agrawal, Sudhir
ITLE OF INVENTION: Modulation of Immunostimulatory Activity of Immunostimulatory
ITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothicate Analogs by
                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITLE OF INVENTION:
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                                                                                                        OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
                                                                                                                                                                                       ENGTH: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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OTHER INFORMATION: modified linkage of oligodeoxynucleotide phosphorothioate
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Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         3 OF INVENTION: Positional Chemical Changes REFERENCE: HYZ-479CP (47508.577)
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/235,452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION
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US20020137714A1
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                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,
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Pred. No.
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Query Match Best Local Similarity

88.9%;

Score 16; Pred. No.

DB 3; 1.4e+02

Length 32;

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APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of
TITLE OF INVENTION: Immunostimulatory
TITLE OF INVENTION: Immunostimulatory
TITLE OF INVENTION: Modulation of Immunostimulatory
TITLE OF INVENTION: Modified oligodeoxynuclectide phosphorothicate Analogs by
TITLE OF INVENTION: Modified oligodeoxynuclectide phosphorothicate Analogs by
TITLE OF INVENTION: Positional Chemical Changes
TITLE OF INVENTION: Wolf of 47508.577)
CURRENT APPLICATION UNMBER: US/10/694,075
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: CURENT APPLICATION NUMBER: US 09/712,898
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
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Publication No. US20040266709A1
GENERAL INFORMATION:
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Best Local Similarity
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Publication No.
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APPLICANT: Zhao, Qiuyan
APPLICANT: Yu, Dong
APPLICANT: Yu, Dong
APPLICANT: Yu, Dong
APPLICANT: Yu, Dong
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Modulation of Immunostimulatory Activity of
TITLE OF INVENTION: Immunostimulatory
TITLE OF INVENTION: Modified olligodeoxynucleotide phosphorothicate Analogs |
TITLE OF INVENTION: Positional Chemical Changes
TILE REFERENCE: HYZ-479CP (47508.577)
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/10/694,075
PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/965,116
PRIOR FILING DATE: CURRENT FILING DATE: 2002-03-08
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Pred. No. 1.4e+02
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                                                                                              US-10-694-383-79
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PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 80
Query Match
Best Local Similarity 87.5
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/235,453
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Immunostimulatory Activity of TITLE OF INVENTION: Modified oligodeoxynucleotide phosphorothicate Analogs by TITLE OF INVENTION: Positional Chemical Changes
FILE REFERENCE: HYZ-479CP (47508.577)
CURRENT APPLICATION NUMBER: US/10/694,383
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION AUMENTE: 2003-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/965,116
PRIOR FILING DATE: CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/712,898
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/235,452
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-11-15
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OTHER INFORMATION:
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                        LOCATION: 16
OTHER INFORMATION: 5'-5' linkage
                                                                                                                                                                                            OTHER INFORMATION: modified linkage of oligodeoxymucleotide OTHER INFORMATION: phosphorothicate
                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                    NAME/KEY: modified_base
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                                                                                                                                                                                                                                                                             TYPE: DNA
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                               88.9%;
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87.5%;
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; Pred. No. 1.4e
2; Mismatches
            Score 16; DB 8;
Pred. No. 1.4e+02
2; Mismatches
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US-10-694-383-80/c
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Best Local Similarity
                                                                                                                                                                                                                                                               equence 79, Apublication No
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PRIOR FILING DATE: CURRENT FILING DATE: 2002-03-08
                                                        CURRENT
                                                                      TLE REFERENCE: HYZ-479CP (47508.577)
URRENT APPLICATION NUMBER: US/10/694,418
                                                                                                           ITLE OF INVENTION:
                                                                                                                                                                                                                          PPLICANT: Kandimalla, Ekambar R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 16
OTHER INFORMATION: 3'-3' linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/235,452
                                 NT FILING DATE: 2003-10-27
APPLICATION NUMBER: US/09/965,116
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FILING DATE: 2003-10-27
                                                                                                                INVENTION: Modulation of Immunostimulatory Activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ
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No. US20040266710A1
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ON NUMBER: US 09/712,898
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                                                                                                             Positional Chemical Changes
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Pred. No.
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LENGTH: 32
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                                                                                                            Query Match
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CURRENT FILING DATE: 2003-10-27
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OTHER INFORMATION: 5'-5' linkage
                                                                                                                                                                                   NAME/KEY: modified_base
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OTHER INFORMATION:
                                                                                                                                                                   OTHER INFORMATION: 3'-3' linkage
                                                                                                                                                                                                                                                                             DRGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                     TYPE: DNA
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ITLE OF INVENTION: Modulation of Immunostimulatory
ITLE OF INVENTION: Modified oligodeoxynucleotide F
ITLE OF INVENTION: Positional Chemical Changes
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                                                                                          Local
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                                                                                            Similarity
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Yu, Sudhir
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                                     AGGGUCGCACGCGGUA 18
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Pred. No.
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Publication No. US20030176376A1

GENERAL INFORMATION:
APPLICANT: RObert B. Klem
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
FILE REFERENCE: 10412-022-999
CURRENT APPLICATION NUMBER: US/10/053,645A
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/263,244
PRIOR PILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
                                                                                                     Query Match
Best Local S
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APPLICANT: Reed, John C.
TITLE OF INVENTION: REGULATION OF BCL-2 GENE
FILE REFERENCE: 04040/1200990-US7
                                                                                 Matches
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PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/961,458
CURRENT FILLING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: US/10/961,458
PRIOR FILLING DATE: 2004-10-07
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 07/288,692
PRIOR FILLING DATE: 1988-12-22
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR FILING DATE: 1993-09-20
PRIOR APPLICATION NUMBER: US 07/840,716
PRIOR FILING DATE: 1992-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of artificial sequence: OTHER INFORMATION: Oligionucleotide
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                                                                                                     y Match 83.3%;
Local Similarity 93.3%;
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; ORGANISM: Homo Sapiens
US-10-756-149-689
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                                                                                                                          ; Sequence 126012, Application US/10424599 ; Publication No. US20040031072A1 ; GENERAL INFORMATION:
                                                                                                                                                                                             US-10-424-599-126012/c
                                                                                                                                                                                                                   RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 689, Applica publication No. US200; GENERAL INFORMATION: APPLICANT: AZIZ, Nat. APPLICANT: Zlotnik,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-756-149-689
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GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: MUMBER: US/10/723,860
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
SOFTWARE: Patentin version 3.2
SQOID NO 668
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.2
SEQ ID NO 689
LENGTH: 337
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Best Local Similarity
Matches 14; Conserv
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Best Local (
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic
TITLE OF INVENTION: Plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 337
TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 93.3%;
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o. US20050181375A1
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Pred. No.
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  Acid
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Thereof for Plant Improvement
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Sequence 34640, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 34640

LENGTH: 381

TYPE: DNA
TYPE: DNA
                                                                                 밁
Search completed: March 19, 2006, 07:52:28
Job time : 2721.85 secs
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US-09-918-995-34640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_84798C.1
US-10-424-599-126012
                                                                                                                                                                                                                                                 GRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 126012
LENGTH: 363
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Local Similarity 93.3%;
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Similarity 93.3%;

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Pred. No. 3.2e+02;
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AA796833 Vp15904.r
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B1333488
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B1548301
O CW553223
B1761653
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CNS01UI
AG0344177
AG038547
BB958176
BG942250
BF978759
BF214752
BG613515
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CD705931
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B1670478
CX760150
BG706282
BUJ941920
BG71855
BUUS96708
B1764038
B1764038
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BE552352
CD693735
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CV569581
CF303740
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BF255098
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             BG706281 602669583
BG722826 602695292
AJ517146 Arabidope
CB960175 AGENCOURT
BU953801 AGENCOURT
BX456870 BX456870
CX755243 AGENCOURT
BX400383 BX400383
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BX540157 Leishmani
CW353224 fsbb001f0
CD685633 RST2154 h
BI548801 603191169
CW353223 fsbb001f0
B1761653 603046382
AV716032 AV716032
BG718649 602696760
B1670478 603294661
CX760159 ACENCOURT
BG706282 60269628
BU941920 ACENCOURT
BG718545 60269628
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CB929313 ABA1 41 H
BE045111 hn28F08.x
BC018628 Homo sapi
BG337115 602434393
R09557 yf27904.81
CA453513 AGENCOURT
CD705931 EST22458
CD698611 EST15134
BU660456 C160c06.z
CR736151 CR736151
CW452151 fsbb001f1
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AL061582 Drosophil
AG034417 Pan trogl
AG03847 Pan trogl
BB958176 601644634
BG942250 ax22h10.x
BF978759 602142290
BP214752 601846671
BG613515 602641444
BG941945 ax19c04.x
AU100090 AU100090
BX115113 BX115113
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BG333304 602431335
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1 (bases 1 to 448)

Marra, M.; Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub. Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Watterston
                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                    The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra Mouse EST Project WashU-HHMI Mouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of Medicinep WashIngton Eark Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                448 bp mRt vp15g04.rl Soares mammary gland NbMMG IMAGE:1068726 5', mRNA sequence.
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Fax: 314 286 1810
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                                              primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 388.
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Brypanosoma; Schizotrypanum.

1 (bases 1 to 759)

1 (bases 1 to 759)

1 Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.

A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery

Genome Res. 10 (12), 1996-2005 (2000)
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                                                                                                                                                                                                                                                                   Seq primer: T7
Class: shotgun.
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Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jul 21, 2000 this sequence version replaced gi:6484020 Contact: Sanchez D.O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ903738.2 GI:9378045
                                                                                                                                                                                                                                                                                                              Email: dsanchez@iib.unsam.edu.ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi
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/clone="G24014"
/cell_type="epimastigote"
/clone lib="Trypanosoma cruzi random genomic library"
/clone lib="Trypanosoma cruzi random genomic library"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb
was gel prified and cloned into the dephosphoryated
was gel prified and cloned into the dephosphoryated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mammary
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                db_xref="taxon:5693"
                                                                                                                                                       /mol_type="genomic DNA"
/strain="CL-Brener"
                                                                                                                                                                                                    organism="Trypanosoma
                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 5.9e+02;
1; Mismatches 1;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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PUIJG38TD ZM_0.6_1.0_KB Zea
                                                                                                                                                                                                      CG117698 854 bp
PUFYD77TB ZM_0.6_1.0_KB Zea mays
T (bases 1 to 854)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
wannick.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                         Zea mays
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Whitelaw,C.A., Quackenbush,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize Genomics Consortium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              el: 301-838-5843
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/clone_ib="ZM_0.6 1.0 KB"
/octes="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
|mol_type="genomic DNA"
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Pred. No. 5.8e+02;
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mayв genomic clone ZMMBTa0596G03,
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea
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                                                                                                                                                          Class: sheared ends
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Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                      mail: whitelaw@tigr.org
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/clone_lib="zm_0.6_1.0_KB"
/clone_lib="zm_0.6_1.0FO; Site_1: EcoRI; 0.6-1.0
/note="Vector: pCr4-TOFO; Site_1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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/clone lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO;
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CoT selected genomic DNA library"
                                                                           /mol_type="genomic DNA"
/strain="B73"
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                                                                db_xref="taxon:4577"
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strain="B73"
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83.3%;
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Pred. No. 5.8e+02;
2; Mismatches 1
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San Miguel,P., Ma,J. an
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a; Poales; Poaceae; PACCAD
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Best Local S
Matches 14
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                                                                              CX774850

841 bp mRNA linear EST 25-JAN-200
UI-EH-HG2-aap-c-17-0-UI.s1 UI-EH-HG2 Emiliania huxleyi cDNA clone
UI-EH-HG2-aap-c-17-0-UI 3', mRNA sequence.
CX774850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anopheles gambiae

Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 730)

Lobo, N.L., Gardner, M., Romans, P. and Collins, F.H.

Anopheles gambiae EST, Center for Tropical Disease Research and
                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18X765851 Normalized Anopheles Fat Body (NAFB gambiae cDNA clone AGCCU12TR, mRNA sequence.

EX765851
     CX774850.1 GI:58
EST.
Emiliania huxleyi
                                                                                                                                                                                                                                                                                                                                      2 GAGGGUCGCACGCGGU 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center for Tropical Disease Research and Training University of Notre Dame Notre Dame, IN 46556, USA Tel: 574-631-9245 Fax: 574-631-3996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Frank H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae (African malaria mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX765851.1 GI:39673060
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="AGCCJ12TR"
//lab host="E. coli DH108"
//lab host="E. coli DH108"
//clone lib="Normalized Anopheles Fat Body (NAFB) Library"
//clone lib="Normalized Anopheles Fat Body (NAFB) Library"
//clone lib="Normalized Anopheles Fat Body (NAFB) Library"
//note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR1 (5'end); Site 2: Not1 (3'end); a
directionally cloned and normalized, oligo-T primed cDNA
library constructed from equal numbers of 24 and 40 hr
post plasmodium inni infection, 4arr and L35 strain adult
female mosquito abdomens (omitting ovaries and midguts):
Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery,
Genome Research 6, 791-806. ESTS sequenced from the M13
reverse priming site reading from the 5' ends of the cDNAs
are indicated by 'R' in the clone name."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frank.h.collins.75@nd.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Anopheles gambiae"
                                                         GI:58185203
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                               88.9%; Score 16; DB 5;
87.5%; Pred. No. 9.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
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Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Fat Body (NAFB) Library Anopheles
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 730;
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                                                                                                                                                       EST 25-JAN-2005
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AUTHORS
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                                                                                                        DEFINITION
                                                                                                                                                       BB081347/c
                                                                                                                                                                                 RESULT
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                                                                                                                                  Snoo
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 15
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PUBMED
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                                                                                                                                                                                                                                                             726
BB081347 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330168K08 3' similar to L07924 Mus musculus guanine nucleotide dissociation stimulator for a ras-related GTPase mRNA, mRNA sequence.

BB081347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Provasoli-Guillard National Center for Culture of Marine Phytoplankton (CCMP)

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/dinoflagellate.html

The following repetitive elements were found in this cDNA sequence: 1-30, >AT rich#Low_complexity (matched compliment)

277-322, SC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                            1 AGAGGGUCGCACGCGG 16
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University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Haptophyceae; Isochrysidales; Emiliania.
1 (bases 1 to 841)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Emiliania huxleyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8889548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    discovery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes vector: p7773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I, Site 2: Not I; UI-EH-HG2 is a polylinker; Site 1: EcoR I, Site 2: Not I; UI-EH-HG2 is a normalized library derived from UI-EH-HG1. The library was constructed and normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAAGGCTAGT. Tissue was obtained from the Provasoli-Guillard National Center for Culture of Marine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytoplankton (CCMP).
TAG_TISSUB=Emiliania huxleyi coccolithophorid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="UI-EH-HG2-aap-c-17-0-UI"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-EH-HG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Emiliania huxleyi"
/mol_type="mRNA"
/strain="CCMP 371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_SEQ=GAAGGCTAGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:2903"
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                                                                                                                                                                                                                                                                                                                                                                                   93.84;
                                                                                                                                                                                                                                                                741
                                                                                                                                                                                                                                                                                                                                                              Score 16; DB | Pred. No. 9.5e | 1; Mismatches
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DB 8; I 9.5e+02;

Length 841;

0

Gaps

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REFERENCE
AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB081347.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermostabilization and thermosctivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          )kazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
9ystem. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [toh,M., Kitsunai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                   prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                   cap-trapper. cDNA
                                                                                                                                       transcriptase and
                                                                                                                                                                           prepared by using trehalose thermo-activated reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="diencephalon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lib="RIKEN full-length enriched, adult male
, Akiyama, J., Shibata, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A.
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                                                                                                   subsequently enriched for full-length by went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for the synthesis of full length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                520-524 (1998)
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duke University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. Analyses of the Chlamydomonas reinhardtii Genome: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ810184.1 GI:22052335
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Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unicellular System for
                                                                                                                                                                                              Similarity
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                                                                            AGAGGGUCGCACGCGGU 17
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                                                                                                                                                                                                                                                                                                                                                                        and Jeffrey McDermott, combines CDNAs from CC-1990 cells which had been re-synthesizing flagella for 15, 30 and 60 min after being deflagellated by pH shock. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. PBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described the control of the lambda cap in the lambda ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; Deflagellation library, constructed by John Davies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="C. reinhardtii CC-1690, Deflagellation
(normalized), Lambda Zap II"
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db_xref="taxon:3055"
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Pred. No. 26
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                                                                                                                                                                                          2e+03;
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                                                                                                                                                                                                                              DB 5;
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RESULT 10

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AUTHORS
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CN122209
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I (bases 1 to 521)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Wylie, T., Dante, M., Ritter, E., Bennett, J., Franklin, C., Tsagaraishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The Washington Univ. Nematode EST Project, 1999

Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                         268 GAGGGACGCACGCGGTA 252
                                                                                                                                                                                                                  CN122209 546 bp mRNA linear EST 01-APR TGESTZY121e08.yl TgVEG118 Tachyzoite cDNA Library-2 Toxoplasma gondii cDNA clone TgESTZy121e08.yl 5', mRNA sequence.
CN122209
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521 bp mRNA linear EST 23-JAN-2002 rr57e03.yl Globodera rostochiensis J2 pcDNAII Smant v1 Globodera rostochiensis cDNA 5' similar to SW:HGD_MOUSE 009173 HOMOGENTISATE
    Tang, K., Co
Clifton, S.,
                                              Sarcocystidae; Toxoplasma.
1 (bases 1 to 546)
                                                                                       Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University Genome Sequencing Center
Seq primer: -40RP from Gibco
High quality sequence stop: 480.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The library was contributed by Dr. Geert Smant of the Lat
Nematology at Wageningen University, Wageningen,
Netherlands(geert.smant@nema.dpw.wau.nl). DNA Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylencholdea; Heteroderidae; Heteroderinae; Globodera.
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Globodera rostochiensis
                                                                                                                                           Toxoplasma gondii
                                                                                                                                                                                              CN122209.1 GI:45943781
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.6%;
larity 88.2%;
Conservative
    Cole,R., Fo
S., Pape,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nematology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Globodera rostochiensis J2 pcDNAII Smant v1"
/note="Vector: pcDNAII (Invitrogen), Site 1: BstXI;
/site_2: EcoRI; The library was donated for sequencing by
Geert Smant from Wageningen University, Laboratory of
Nematology, The Netherlands."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:31243"
/dev_stage="J2"
/lab_host="DH10B"
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Fogarty, S., Si
D., Martin, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; D
Pred. No. 2e+0
1; Mismatches
  Sibley,L.D., Ajioka,J.A., White,M., ., Wylie,T., Dante,M., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 521;
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                                                                                                                                                                                                                                                                                        EST 01-APR-2004
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AUTHORS
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SOURCE
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Best Local S
Matches 14
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Contact: Clifton, S. Toxoplasma EST Project Post Resident Clifton, S. Toxoplasma EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810

Fax: 314 286 1810
                1 (bases 1 to 600)

WCCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucha, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Onter: McCann, R., Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                      Globodera rostochiensis
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
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BM355249.1
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600 bp mRNA linear EST 23-JAN-200:
rr22f03.yl Globodera rostochiensis J2 pcDNAII Smant v1 Globodera
rostochiensis CDNA 5' similar to SW:HGD_MOUSE 009173 HOMOGENTISATE
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Location/Qualifiers
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Contact: McCarter JP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: toxo@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="TgVEG118 Tachyzoite cDNA Library-2"
/note="Vector: pBluescript SK; Site 1: ECCR1; Site 2:
XhoI; The library was constructed by Kellang Tang, Robert
Cole and L.David Sibley at Washington University. cDNAs
were synthesized from poly(A)+ RNAby oligo d(T) printing,
size-selected and directionally cloned into the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemids and rescued in SOLR cells. The
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/dev_stage="Tachyzoite"
/lab_host="GC10"
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/strain="VEG"
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/mol_type="mRNA"
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Pred. No. 2e+03;
2; Mismatches 1; Indels
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Nematode EST Project, 1999

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other GSSs: Sheared DNA-49A17.TR
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ946516 614 bp DNA linear GSS 27-JAN-20 Sheared DNA-49A17.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-49A17, genomic survey sequence.
                                                                                                                                                    Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/. Seq primer: M13-Forward Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C. Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M. Determination of clone end sequences from Trypanosoma brucei GUTat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma brucei
Trypanosoma brucei
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The library was contributed by Dr. Geert Smant of the Laboratory of
Nematology at Wageningen University, Wageningen,
Netherlands(geert.smant@nema.dpw.wau.nl) DNA Sequencing by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
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Location/Qualifiers
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/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;
Site_2: EcoRI; The library was donated for sequencing by
Geert Smant from Wageningen University, Laboratory of
/organism="Trypanosoma brucei"
/mol type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
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v_stage="J2"
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Pred. No. 2e+03;
1; Mismatches 1; Indels
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P., Ullu,E., Melville,S.,
                                                                                                                                                                                                                                                                                                                                                                                            MD 20850, USA
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Best Local
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Other GSSs: Sheared DNA-43M6.TR
Contact: Najib M. E1-Sayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,B., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,B., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
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AQ953132.1 GI:6776397
GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Bukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Sheared DNA-49A17"
/clone lib="Sheared DNA"
/clone lib="Sheared DNA"
/note="Vector: pUC18; Site 1: Smal; Constructed at
Institute for Genomic Research (TIGR), Rockville, M
sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
                                                                                                                                      Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
                                                                                                                                                                                                                            /clone_lib="Sheared DNA"
/note="Vector: pUC18; Site_1: SmaI; Constructed at The
/notte="Vector: puc18; Site_1: SmaI; Constructed at The
/notte: puc18; Site_1: SmaI; Site_1: SmaI
                                                                                                                                                                                                                                                                                                                                                    /mol type="genomic DNA"
/strain="TREU927/4 GUTat 10.1"
/db xref="taxon:5691"
/dlone="Sheared DNA-43M6"
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82.4%;
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RESULT 16
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Best Local Similarity
Matches 14; Conserv
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       BJ650743
BJ650743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go-jp, URL:http://hgp.gsc.riken.go-jp/, Tel:81-45-503-9111, Pax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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R.Site 1 : SacI
R.Site 2 : SacI.
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713
Eptatretus burgeri a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                    /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                           organism="Pan troglodytes"
                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-080L03.R"
                                                                                                                                                               85.6%;
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Pred. No. 2e+03;
2; Mismatches 1;
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Pred. No. 2
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     adult
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. 2e+03;
       Eptatretus
                    mRNA
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                                                                                                                                                                            Length 667;
                   linear
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       burgeri
       EST 07-OCT-2004
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Matches
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Eptatretus burgeri (inshore hagfish)
Eptatretus burgeri
Eptatretus burgeri
Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
1 (bases 1 to 752)
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30550743

BJ650743.1 GI:53865604

EST.

Eptatretus burgeri (inshore hagfish)

Eptatretus burgeri

Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;

Myxinidae; Eptatretus.

1 (bases 1 to 713)

Suzuki, T.; Shin-I,T.; Kohara, Y. and Kasahara, M.
                                                                                                                                                                                                                                                                                                                                     Suzuki, T., Shin-I,T., Kohara,Y. and Kasahara,M.
Transcriptome analysis of hagfish leukocytes: a framework
understanding the immune system of jawless fishes
Dev. Comp. Immunol. 28 (10), 993-1003 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ662705 Eptatretus burgeri adult Eptatretus burgeri cDNA clone
hg121106 3', mRNA sequence.
BJ662705 BJ662705 GI:53877568
EST.
                                                                                                                                                                                                                 Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptome analysis of hagfish leukocytes: a framework understanding the immune system of jawless fishes Dev. Comp. Immunol. 28 (10), 993-1003 (2004)
                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                     Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
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Location/Qualifiers
/organism="Eptatretus
/mol_type="mRNA"
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/clone="hg121h06"
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/mol_type="mRNA"
/db_xref="taxon:7764"
/clone="hg121h06"
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/dev_stage="adult"
/clone_lib="Eptatretus burgeri adult"
/note="wild caught animal"
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Pred. No. 2e+03;
1; Mismatches 1;
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RESULT 18
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                                                                                DR729209 770 bp mRNA linear EST 15-AGENCOURT_55139068 NICHD_XGC_Emb9 Xenopus laevis cDNA clone MAGE:7978626 5', mRNA sequence.
Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osada, S., Kitayama, A., Ueno, N. and Taira, M. Expression analysis of genes which are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                   DR729209.1 GI:70903321
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'enopodinae; Xenopus; Xenopus.

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                                                                                                                                                                                                                                GAGGGUCGCACGCGGUA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cience and Technology Corporation, Japan
-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Ja
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           m_taira@biol.s.u-tokyo.ac.jp,
tp://www.shigen.nig.ac.jp/nbrp/xenopus/est/
                                                                                                                                                                                                                                                                                                                                             /dev_stage="late gastrula (stage 12.5)"
/clone_lib="Osada Taira anterior neuroectoderm
pCS105 cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/clone_lib="Eptatretus burgeri adult"
/note="wild caught animal"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="anterior neuroectoderm"
                                                                                                                                                                                                                                                                                                                                                                                                                clone="XL445e24ex"
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BST.
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenomodinae; Yanomus. Yanomus
Graduate School of Science, University of Tokyo; Science and Technology Corporation, Japan 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                          Contact: Masanori Taira
Department of Biological Sciences
                                                                                                                                                                                                               1 (bases 1 to 771)
Osada, S., Kitayama, A., Ueno, N. and Taira, M.
Expression analysis of genes which are expressed in the anterior
                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                        Unpublished (2004)
                                                                                                                                                                              neuroectoderm of Xenopus embryos
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Kenopus laevis (African clawed frog)
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Similarity 88.2%;
                                                                                                                                                                                                                                                                                                         kenopodinae; Kenopus; Kenopus
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/clome_lib="NICHD_XGC_Emb9"
/note="Organ: embryo; Vector: pExpress-1; Site_1: EcoRV;
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clone="IMAGE:7978626"
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mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University in St. Louis
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2004)
Contact: Mitreva M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Waterston,R.H., Clifton,S.W. and Wilson,R.
Genome Survey sequences from the parasitic nematode Ancylostoma
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                                                                                                                                                                                                                                                                                                                                                                                                Email: nematode@watson.wustl.edu
Genomic DNA provided by John Hawdon
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostoma.
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Ancylostoma caninum
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Fax: 81-03-5841-4434
                                                                                                                                                                                                                                                                                                                                                                           sequenced by Washington University Genome
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                Ancylostoma caninum genomic DNA was randomLy sheared, end-repaired and size fractioned to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjmlægwunc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing center, St. Louis, MO."
                                                                                                                                                                                                                                                                                                                     1. .812
                                                                                                                                                                                               /db_xref="taxon:29170"
/dev_stage="Adult"
/lab_host="GS10"
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/dev_stage="late gastrula (stage 12.5)"
/clone_lib="gada Taira anterior neuroectoderm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL468m17ex"
                                                                                                                                                       clone_lib="Ancylostoma caninum whole genome shotgun ibrary (AIAAGSS 001)"
                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="Baltimore"
                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                organism="Ancylostoma caninum"
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88.2%;
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                                                                                                         CV762975 926 bp FGAS057364 Triticum aestivum FGAS: aestivum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs romail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM.14206 row: 1 column: 10
                                                       Bestivum cDNA, mRNA seq
CV762975
CV762975.1 GI:55604086
EST.
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AGENCOURT 10487935 NICHD XGC Embl
IMAGE:6634258 5', mRNA sequence.
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                   Triticum aestivum (bread wheat)
Triticum aestivum
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Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU908733
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                                                                                                                                                                                                                                                                                                                                   h 85.6%; Score 15.4; DB 5; Length 906; Similarity 88.2%; Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:6634258"
/tissue_type="embryo (stage 10)"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NICHD_XGC_Emb1"
/clone="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned_unidirectionally. Primer: Oligo dT. Average insert size_1.55 kb. Constructed by Life_Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                            1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05D14 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Eukaryota, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

[ (bases 1 to 1101)
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Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Linke, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F. Functional Genomics of Abiotic Stress In Wheat and Canola Crops
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was
collaboration with the Berkeley Drosophila
The BDGP is constructing a physical map of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
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Contact: Wm L Crosby
                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (B-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: fgas_ests@cs.usask.ca
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                                                                                                                                                            Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                        AL061582.1 GI:4939944
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Similarity 82.4%;
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ce: WEF032 row: C
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/note="Organ: Crown and leaf; Vector: pCMV.SpORT6; Aerial
parts (crown and leaf) of wheat cultivar Norstar from
control and long exposure times to low temperature. 4 mRNA
populations were combined before constructing the library;
7 days non-acclimated plants and 1, 23, and 53 days
cold-acclimated at 4C. Non-acclimated and cold-acclimated
plants were grown in vermiculite This is the only library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that was done according to the Invitrogen manual, and therefore, a percentage of clones will not have the 3 prime end because of NotI digestion within the cDNA."
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/db_xref="taxon:4565"
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  Carried out as
Genome Project
the Drosophila
                                                                                                         segref@genoscope.cns.fr
                                                                                                                                     National de Sequencage
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                                                    part of a
                                 (BDGP).
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                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (R-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  rujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                        Sequencing: -21M13
LIBRARY
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                                                                                                                       R.Site 1
R.Site 2
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/mol_type="genomic_DNA"
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/clone="BACR05D14"
/clone_lib="RPCI-98"
/note="end : TET3"
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                            Location/Qualifiers
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: SacI
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ne: PTB-009M03.F, genomic survey sequence.
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RESULT 27
BE958176
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Best Local Similarity
Matches 14; Conserv
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                                                                                                               1136
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BE958176 99 bp mRNA linear EST 04-OCT-2000 601644634F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929792 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-2001) Asao Pujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Pax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1310
Pan troglodytes DNA, clone: P
AGG38547
                                                                                                                                          2 GAGGGUCGCACGCGGUA 18
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                       Similarity
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                                                                                                           GAGTGTCGCACGCGGTA 1152
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R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                clone="PTB-015G04.F"
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Pred. No. 1.9e+03;
2; Mismatches 1
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Pred. No. 2e+03;
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PTB-015G04.F,
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genomic
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SOURCE
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Best Local Similarity 93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 bp mRNA linear EST 15-JAN-2003 ax22h10.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens cDNA clone ax22h10 random, mRNA samanan BG942250
                                                                                  1 (bases 1 to 108)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG942250.1 GI:14341622
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
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/note=Torgan: brain; Vector: pDNR-LIB (Clontech); Site_1:
/note=Torgan: brain; Vector: pDNR-LIB (Clontech); Site_1:
/note=Torgan: brain; Vector: power and content a
Jeffery L. Miller
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_56"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3929792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 99
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Pred. No. 3.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                         602149290F2 NIH_MGC_62 Homo sapiens
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Intramural Sequencing Center (NISC).
Plate: 22 row: h column: 10
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                       BF978759.1 GI:12345974
                                                                                                                                                                                                                                                                                                                                                                   BF978759
                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 402 2373
Fax: 301 435 5148
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                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                             Email: cgapbs-r@mail.nih.
                                                                                                                                                                    Hominidae; Homo.
1 (bases 1 to 132)
                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.nisc.nih.gov/)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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'lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell_type="Brythroid Cells"
cell_line="Primary Culture of Peripheral Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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ement: ATCC/DCTD/DTP
Preparation: CLONETECH Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lib="Hembase; Erythroid Progenitor Cells (LCB:ax
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Pred. No. 3.3e+03;
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National Institutes of Health, Bethesda,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 149)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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BF214752.1
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601846671F1 NIH_MGC_55
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Plate: LLCM1179 row: c column: 24
                                                                                                                                       http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM933 row: m column: 17
Plate: LLCM933 row: m column: 17
High quality sequence stop: 149.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                  cDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.I.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/lab_host="DH10B (Tl phage-resistant)"
/clone_lib="NH1MGC_62"
/clone="Torgan: skin; Vector: pDNR-LIB (Clontech); Site_l:
/note="Torgan: skin; Vector: pDNR-LIB (Clontech); Site_l:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCGATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTMCAGGGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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                       /db_xref="taxon:9606"
/clone="IMAGE:4077880"
                                                                                              organism="Homo sapiens"
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tissue_type="from acute myelogenous leukemia"
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Pred. No. 3.3e+03
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602641444F1 NIH_MGC_61 Homo sapiens
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG613515.1 GI:13664886
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Similarity 93.3%;
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/tissue_type="embryonal carcinoma"
/lab host="DH108 (T1 phage-resistant)"
/clone lib="NH108 (Clontech); Site_1:
/clone lib="NH108 (Clont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 55"
/clone lib="NIH MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (gyccgcctcggcc); Site_2: SfiI
(gyccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5' CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5' -ATTCTAGAGCCGAGGCGGCCGACGTCTC-dT(30)BN-3' (where B = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4772411"
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Pred. No. 3.3e+03;
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ORGANISM
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BG941945
LOCUS
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VERSION
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intramural Sequencing Center (NISC).
Plate: 19 row: c column: 04
Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7f@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 197)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG941945 197 bp mRNA linear EST 15-JAN-ax19c04.x1 Hembase; Erythroid Progenitor Cells (LCB:ax library) Homo sapiens cDNA clone ax19c04 random, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Jeffery L. Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10409428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing and analyses by National Institutes of Health
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/note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: EcoRI; 65,000 proliferating crythroid cells from the Euffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of crythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                             /cell type="Erythroid Cells"
/cell line="Primary Culture of Peripheral Blood
Monomcolear Cells"
/dev stages"Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library."
                                                                                                                                                                                                                                                                                                                                                                 library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="ax19c04"
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RESULT 34
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AU100090
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                                                            SOURCE
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                                                                                                                                                          DEFINITION
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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BX115113 Soares_testis_NHT Homo
; IMAGE:728071, mRNA sequence.
                                                                                                                                                                                                                                                                                      N
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Suzuki,Y., Tsunoda,T., Sese,J., Taira,H., Mizushima-Sugano,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Suyama,A., Sakaki,Y., Morishita,S., Okubo,K. and Sugano,S. Identification and characterization of the potential promoter regions of 1031 kinds of human genes
Genome Res. 11 (5), 677-684 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU100090 300 bp mRNA linear EST 23-JAN AU100090 Sugano Homo sapiens cDNA library Homo sapiens cDNA clung06538 similar to Human mitochondrial transcription factor 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jaj
                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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AU100090.1 GI:13551219
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                           BX115113.1
                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                            sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Sugano Homo sapiens cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="LNG06538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                           GI:27879949
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93.3%;
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                                                                                                                                                                                                                                                                                                                      Score 15; DB
Pred. No. 3.3e
1; Mismatches
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Pred. No. 3.3e+03;
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3.3e+03;
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sapiens
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                                                                                                                                                          CDNA
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kamura, Y., Suyama, A.,
                                                                                                                                                        linear
NA clone
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                                                                                                                                                                                                                                                                                        DEFINITION
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                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                     RESULT 35
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                                                                                                                                                                                                                                                                                                                      AA393273
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Matches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                                                                                                                                                                       237 bp mRNA linear EST 12-AUG-1997 t74044.rl Soares testis NHT Homb sapiens CDNA clone IMAGE:728071 5' similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (HUMAN);, mRNA sequence.
                 1 (bases 1 to 337)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Kucaba,T., Lacy,M., Le,N., Lemnon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RZPD; IMAGD998F081786.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human UnigeneSet -
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                               Homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                          AA393273.1 GI:2046241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung Gmb
                                                                                                                                                                                                                        Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de
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Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cots, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Soares testis NHT"
/notes="Vector: pT/T30-Pac (phasmacia) with a modified
/notes Vector: pT/T30-Pac (phasmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"

mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="IMAGp998F081786; IMAGE:728071"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15; DB 5;
Pred. No. 3.3e+03;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 314;
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SOURCE
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BM851628
                                                                                                                                                                                                                                           COMMENT
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                                               FEATURES
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                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 GAGGGTCGCACGCGG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                             Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                           1 (bases 1 to 349)

Kim, N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Prontier Korean EST Project 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                          Email: yongsung@mail.kribb.re.kr
Plate: 44 row: D column: 04
High quality sequence stop: 349.
                                                                                                                                                                                                                                         Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K-EST0132545 S13KMS5 Homo sapiens cDNA clone S13KMS5-44-D04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1084 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM851628.1 GI:19208027
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h quality sequence stop: 163.
   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_testis_NHT"
/note="Vector: py773D-Pac (Pharmacia) with a modified
/note="Vector: py773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I, Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                            Location/Qualifiers
/organism="Homo sapiens"
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/mol_type="mRNA"
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                          .349
                                                                                                                                                                                                                                                                  (2002)
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 06-MAR-2002
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CW842063/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Tosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CW842063 376 bp DNA linear GSS 26-PET11920.Ds3.04.14.2003.jw95.376 Arabidopsis thaliana Landsbeinsertion lines Arabidopsis thaliana genomic clone ET11920,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                        Email: martiens@cshl.org
This sequence flanks a Ds transposon carrying an enhancer trap
line ET11920. The transposon is located upstream of At1g72290.
Nucleotides 1. .32 are derived from Zea mays transposon Ds.
                                                                                                                                                                                                                                                                                                                                                                      Tel: 516 367 8322
Fax: 516 367 8369
                                                                                                                                                                                                                                                                                                                                                                                                                          Cold Spring Harbor Laboratory
1 Bungtown Rd., Cold Spring Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 376)
May, B.P., Simorowski, J., Arroyo, J.-M., Vaughn, M.W., Shen, R., McCombie, W.R. and Martienssen, R.A.
Arabidopsis genomic sequences flanking Ds enhancer and gene in transgenic lines
Unpublished (2004)
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                                                                                                                                                                                                                                          Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Martienssen RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell line="KMS-5"
/lab_host="Top10F"
/lab_host="Top10F"
/lab_host="Top10F"
/clone lib="813KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
/note="Vector: pCNS; Site_1ted with bacterial alkaline
phosphatase (BAP) and then decapped with tabacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dT-selected mRNA by priming with
dT-tailed vector. The dT-tailed vector was adjusted to
have about 60nt. The cDNA vector was acircularized with E
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
/clone_lib="Arabidopsis thaliana Landsberg Ds insertion
lines"
                                                                          /ecotype="Landsberg erecta"
/db_xref="taxon:3702"
                                                                                                                              organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="myeloma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="S13KMS5-44-D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 3;
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             Harbor,
                                                                                                                                                                                                                                                                                                                                                                                                                                NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ds enhancer and gene traps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 26-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Length 396;

: EST 08-JUN-2000 IMAGE:3023463 3'

```
Other_ESTs: ABA1 41_H09.b1_A012
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and Rusuki at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB929313 396 bp mRNA linear ABA1_41_H09.g1_A012 Abscisic acid-treated seedlings CDNA clone ABA1_41_H09_A012 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D., Eastman, A. and Pratt, L.H.
An EST database from Sorghum: ABA1-treated seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 706 542 1860 Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB929313.1 GI:30165584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
Library constructed by Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGTCGCACGCGGT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGUCGCACGCGGU 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                      /clone lib="Abscisic acid-treated seedlings"
/note="Vector: pME185-FL3; Site_1: XhoI; Site_2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. After 12 days, medium was
supplemented with 1 mM abscisic acid (ABA), while leaves
were misted with a solution of 1 mM ABA. Roots and leaves
were misted with a solution of 1 mM ABA. Roots and leaves
were harvested after 3, 6, 12, and 24 hr and material from
all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
different brail sites of the pME185-FL3 vector (5-prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Lines of Arabidopsis thaliana were generated which each contain a Ds transposon carrying a glucuronidase reporter gene. Genomic DNA flanking the transposon insertion in each line was amplified by PCR and directly sequenced. More information is available at http://genetrap.cshl.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:4558"
/clone="ABA1 41 H09 A012"
/lab_host="DH10B-T1 phage-resistant E. coli"
                                                                                                                                                                                                                                                                                                                                                                                           cultivar="IS3620C"
                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sug5 (CTTCTGCTCTAAAAGCTGCG).
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                                                                                                                                                                                                                                                                                                                                                                                                                    type="mRNA"
site is CACTGTGTG, 3-
GTG). XhoI excises the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15; DB 10;
Pred. No. 3.2e+03;
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     DraIII site is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 28-APR-2003
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                        RESULT 40
BC018628
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AUTHORS
TITLE
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VERSION
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BE045111
LOCUS
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                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                     Matches
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                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hn28f08.x1 NCI CGAP Thy7 Homo sapiens cDNA clone IMAGE:3023463 3' similar to gb:M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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  BC018628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE045111
BE045111.1 GI:8362164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible reversed clone: poly
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Klaus Kaserer M.D., Bruno Niederle M.D.,
Emmert-Buck M.D. Ph.D.,Vlado Knezevic M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Krizman Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
                                                                                                                             GAGGGTCGCACGCGG 34
                                                                                                                                                                              GAGGGUCGCACGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 412)
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                      agarose gel, average insert size 500 bp. Primary library.

CDNA Library Preparation: David B. Krizman, Ph.D.

REFERENCE: Krizman et al (1006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCI CGAP Thy7"
/note="Organ: thyroid; Vector: pAMP10; mRNA made from thyroid adenoma (benign), cDNA made by oligo-dT primi Non-directionally cloned into UDG sites. Size-selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'tissue_type="follicular adenoma (benign lesion)"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                           93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 6;
Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                           Score 15; DB 2;
Pred. No. 3.2e+03
                                                                                                                                                                                                                                  Mismatches
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413 bp
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  mRNA
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Mike

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REFERENCE AUTHORS

COMMENT

JOURNAL TITLE

FEATURES

source

0; Indels

Gaps

linear

HTC 06-DEC-2001

Length 412;

· Sutuntad

ACCESSION VERSION

SOURCE **EYWORDS** 

ORGANISM

RESULT 38 CB929313/c

DEFINITION

S

96

Matches

Best Local Similarity

ORIGIN

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RESULT 41
BG337115
                        SOURCE
ORGANISM
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VERSION
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AUTHORS
TITLE
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                                                              KEYWORDS
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                   16
                                                                                BG337115
BG337115.1
                                                                                                                                                                                                                                                                                                      2 GAGGGUCGCACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                BG337115
602434393F1_NIH_MGC_46 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Series: IRAL Plate: 40 Row: d Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4507
This clone has the following problem: frame shifted.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens, Similar to transcription factor A, mitochondrial, clone IMAGE:4552415, mRNA.
BC018628
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
1 (bases 1 to 413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                 GAGGGTCGCACGCGG 30
                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                           note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_46"
/lab_host="DH10B_R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:4552415"
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                                                                                   GI:13143553
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93.3%;
                                                                                                                                                                                                                                                                                                                                                                Score 15;
Pred. No.
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                                                                                                                                                             414
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                                                                                                                                                                                                                                                                                                                                        .2e+03;
                                                                                                                                                               mRNA
                                                                                                                                           cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                   Length 413;
                                                                                                                                         ear EST 27-FEB-2001
IMAGE:4552415 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA gi: 4507400
    Euteleostomi;
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VERSION
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R09557
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AUTHORS
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                                                                                                   TITLE
JOURNAL
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Best Local
                                                                                                                                                                                                                       AUTHORS
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                         R09557
Yf27g04.81
                                                                                                 The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                R09557.1 GI:761480
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 4
High quality sequence stop: 413.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE:128118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.
1 (bases 1 to 414)
                                                                                                                                                                                                                                                               Hominidae; Homo.
                                                                                                                                                                                                                                                                                  Mammalia; Butheria;
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                    3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
93.3%;
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1 (bases 1 to 426)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/db xref="taxon:9606"
/clone="IMAGE:4552415"
/tissue_type="lelomyosarcoma cell line"
/lab host="NIH_MGC_46"
/clone_lib="NIH_MGC_46"
/clone_lib="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426 bp mRNA
Soares fetal liver spleen infls
                                                                                                                                                                                                                                                                                                                                                                                                                      Euarchontoglires;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 3.2e+03;
1; Mismatches 0
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                                                                                                                                                   Marra, M.,
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RESULT 43
CA453513
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AUTHORS
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ORGANISM
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 bp .n
AGENCOURT 10578892 NIH_MGC 127 Homo
IMAGE:6717438 5', mRNA BEQUERICA
CA453513
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                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 429)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Insert Length: 817 Std Error: 0.00
                                                                   http://image.llnl.gov
Plate: LLCM3034 row: c column: 06
High quality sequence stop: 409.
                                                                                                                                                                                                                                                                   Tissue Procurement: NCI
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="20 week-post conception fetus"
(lab_host="DH10B (ampicillin resistant)"
(clone_lib="Soares fetal liver spleen INFLS"
(rotee="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Homo sapiens"
'mol_type="mRNA"
'db_xref="GDB:480279"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
organism="Homo sapiens"
                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one="IMAGE:128118"
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Pred. No. 3.2e+03;
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2; Mismatches
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RESULT 44
CD705931
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DEFINITION
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Matches 14
Query Match
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Matches 14
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EST22458 human nasopharynx Homo
CD705931
                                                                                                                                                                                                                                                                                                                           Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Contact: YiXin Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD705931.1 GI:32236561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iu, X.-Q., Zhou, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGGUCGCACGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 463)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                            86-20-8775-4506
                                                                                                                                                                                                                                                           yxzeng@gzsums.edu.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clome_lib="NIH_MGC_127"
/note="Vector: pDNR-LB; Site_1: SfiI (ggccattatggcc);
/note="Vector: pDNR-LB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcttggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
-2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon
-2%, blood - 33.4%, brain - 5.6%, intertine - 2.6%
                                                                                                    'tissue type="normal nasopharynx"
(clone Tib="human nasopharynx"
note="ESTs generated from a normal nasopharynx cDNA
(ibrary from southern Chinese"
                                                                                                                                                                                                    organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="mixed (pool of 40 RNAs)"
[lab_host="DH10B (T1-phage-resistant)"
                                                                                                                                                                                     db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Euarchontoglires; Primates; Catarrhini;
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                   83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G.
  Score 15; DB 6;
Pred. No. 3.2e+03;
1; Mismatches 0
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Pred. No. 3.2e+03
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sapiens cDNA,
                                        Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
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GAGGGTCGCACGCGG 63 GAGGGUCGCACGCGG 16

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REFERENCE
AUTHORS
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ACCESSION
VERSION
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BU660456
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AUTHORS
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CD698611
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                                                                                                                                                                                  COMMENT
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                             1 (bases 1 to 492)
Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
Gene Expression in Human Erythroid Precursor Cells
Unpublished (2002)
Tel: 301 402 2373
Pax: 301 435 5148
Email: jm/fenih.gov
The 'cl' library was constructed by Alexander Gubin, Ph.D.
Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing
                                                                                                                    Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                       8U660456 492 bp mRNA linear EST 30-SEP-
C160C06.z1 Hembase; Erythroid Precursor Cells (LCB:cl library)
sapiens cDNA clone c160c06 5', mRNA sequence.
BU660456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GAGGGUCGCACGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 bp
EST15134 human nasopharynx Homo
CD698611
CD698611.1 GI:32227094
                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yxzeng@gzsums.edu.cn.
Location/Qualifiers
1. .487
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Cancer Center
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                         Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                      BU660456.1 GI:23372638
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                                                                                                      20892,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DongFeng Road East,
: 86-1380-9770-743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yat-sen University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86-20-8775-4506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scriptional Gene Expression Profile of Human Nasopharynx
blished (2003)
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                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 6;
Pred. No. 3.2e+03;
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sapiens cDNA, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 487;
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         in the and/or
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TITLE
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SOURCE
ORGANISM
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AUTHORS
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VERSION
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CR736151
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 493)

Ebert, L., Heil, O., Hennig, S., Korn, B., Peters, M., Radelof, U. and Schneider, D.

I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at: http://hembase.niddk.nih.gov Plate: 60 row: c column: 06 Seq primer: 5' lambda-TriplEx2 Sequencing Primer.
                                         Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGp998B164415.
RZPDLIB; I.M.A.G.B. CDNA Clone Collection;
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR736151

CR736151 Soares testis NHT Homo sapiens cDNA clone IMAGp998B164415

IMAGE:1737519 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GAGGGUCGCACGCGG 16
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CR736151.1 GI:51586228
                    RZPDLIB; I.M.A.G.E. (Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Deutsches Ressourcenzentrum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; Http://www.nisc.nih.gov/)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Hembase; Erythroid Precursor Cells (LCB:cllbrary)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (N-terminal) -biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
(N-terminal) -biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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|cell_line="Primary Culture of Peripheral Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="cl60c06"
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93.3%;
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Pred. No.
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fuer Genomforschung GmbH
                                                                                                                                                                                                                                                                        Neubert, P., Partsch, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 492
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RESULT 48
CW452151/c
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       FEATURES
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CW452151 530 bp DNA linear GSS 02-NC fsbb001f192i20f0 Sorghum methylation filtered library (LibID Sorghum bicolor genomic clone fsbb001f192i20, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                   Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: fsbb001ff192 row: i column:
                                                                                                                                                                                                   Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                               Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robb Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMennamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., K Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 530)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
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                                                                            Seq primer: f Forward
                                                                                                                                                                                                                                                 Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW452151.1 GI:55200112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.rzpd.de
                                                                                                                                                                                                                                                                                15660154
                                                                                                                                                                                                                                                                                                                                                  Martienssen,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGGTCGCACGCGG 313
lass: methylation filtered
igh quality sequence stop: 530.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
/clone lib="Soares testis NHT"
/clone lib="Soares testis NHT"
/note="Vector: puTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratories, Inc., and primed with a Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
|mol_type="mRNA"
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clone="IMAGp998B164415 ; IMAGB:1737519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%;
93.3%;
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Pred. No.
                                                                                                                                                                                                   St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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RESULT 49
CB138822
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DEFINITION
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AUTHORS
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VERSION
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CB138822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB138822
K-EST0191737 L5HLK1 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 546)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB138822.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yongsung@mail.kribb.re.kr
Plate: 36 row: B column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21C Frontier Korean EST Project 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGGUCGCACGCGG 16
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                   /note=Worgan: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end-repaired, size fractionated to enrich for the 0.5 to kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation filtered library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared
                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                  clone="L5HLK1-36-B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="fsbb001f192i20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.3%;
93.3%;
                                                                                                                                                                                                                                                        host="Top10F'"
ne_lib="L5HLK1"
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                                                                                                                                                                                                                                                                                                         line="HLK-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 10;
Pred. No. 3.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
i DNA ligase after digestion of included in vector. An RNA stra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 29-JAN-2003
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  An RNA strand
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ORGANISM
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VERSION
KEYWORDS
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BE552352/c
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                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hy06e05.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3196544 3' similar to gb.M62810 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (HUMAN), mRNA sequence.

BE552352
BE552352.1 GI:9794044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 481.
Location/Qualifiers
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2 GAGGGUCGCACGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAGGGUCGCACGCGG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.
1 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGTCGCACGCGG
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ilarity 93.3%; Pred. No. 3.2e+03;
Conservative 1; Mismatches 0;
                                                                                                                                                                  /clone lib=WCI CGAP GC6"
/clone lib=WCI CGAP GC6"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI—GGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:3196544"
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APPLICANT: Krieg, Arthur M.

APPLICANT: Schwartz, David A.

ITILE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING

ITILE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING

ITILE OF INVENTION: LPS-ASSOCIATED DISORDERS

FILE REFERENCE: C1039/7011

CURRENT APPLICATION NUMBER: US/09/030,701B

CURRENT FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/039,405

PRIOR APPLICATION NUMBER: 60/039,405

PRIOR APPLICATION NUMBER: 50/039,405

PRIOR FILING DATE: 1997-02-28

NUMBER OF SEG ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 28

LENGTH: 18
                               RESULT 2
US-09-286-098-60/c
US-09-286-098-60/c
; Sequence 60, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: synthetic oligonucleotide US-09-030-701-28
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US-09-030-701-28/c
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Patent No. 6214806
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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US-10-011-146-1
US-09-902-540-4681
US-09-949-016-5637
US-10-160-719A-13
US-10-160-719A-21
US-10-160-719A-21
US-10-160-719A-21
US-10-209-059-45
US-09-332-522E-7
US-08-506-296B-20
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US-08-793-198-8
US-08-793-198-8
US-08-793-641-8
US-08-617-697-7
US-08-793-824-1
US-08-793-824-1
US-08-793-824-1
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                                                                                                                                                                                                                                                           Score 18;
                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                        DB 3;
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21, Appl
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; MOLECULE TYPE:
US-08-960-774-60
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US-08-960-774-60/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 619/678-5070
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TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines
FILE REFERENCE: Cl039/7026/HCL
CURRENT PILING DATE: 1999-04-02
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOPTMARE: PastSEQ for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: THEORYTING CONTINUES OF SECURE OF SE
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Patent No. 6239116
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Best Local Similarity
Matches 16; Conserv
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                  LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 92037
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STATE: CA
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88.9%;
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Score 18; DB 3; Pred. No. 5.7;
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Pred. No. 5.7;
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                                          Length 18;
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JS-09-191-170-54/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               09-337-619-60/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                             ent No.
HER INFORMATION: Synthetic Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54,
                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/738,652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/191,170
                                                                                                                                                     APPLICATION NUMBER: US 08/276,358
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                                                                                                                                                                                                                                                                                                                        INVENTION: Methods of Treating Cancer Using INVENTION: Immunostimulatory Oligonucleotides
                                                                                                                                                                                                                                                    PPLICATION NUMBER: US 08/960,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                   FastSEQ for Windows Version 3.0
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                                                                                                                                                                                    US 08/386,063
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                                                                                                                                                                                                                                                                                                                                           US-08-465-485A-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic oligonucleotide US-09-954-987B-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URRENT APPLICATION NUMBER: US/09/954,987B
URRENT FILING DATE: 2001-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
   JURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                         STREET:
                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/263,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/300,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/291,726
                                                                                                                                                     TY: Arlington
                                                                   TER READABLE FORM:
TYPE: Floppy
                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                           , Application US/08465485A 5831066
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                                                                                                                                       Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09954987B
                                                                                                                                                                     1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                 IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C1041/7016 (AWS)
                                                                                                                                                                                                      OBLON, SPIVAK, McCLELLAND,
                                                                   Floppy dis
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                                                                                                                                                                                                                                                        Regulation of bcl-2 Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipford
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                   Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ.
                   Version #1.25
                                                                                                                                                                                                       MAIER & NEUSTADT,
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APPLICATION NUMBER: FILING DATE: 05-JUN CLASSIFICATION: 514

05-JUN-1995

US/08/465,485A

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Query Match
Best Local Similarity
Matches 15; Conserve
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US-09-080-285-9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09080285 Patent No. 6040181
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION NUMBER: US 07/840,716
APPLICATION NUMBER: US 07/840,716
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 22-DEC-1988
                                                                                                                                                                                          MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bc1-2 Gene Expression
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ANTI-SENSE: YI
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: FORTHEY, Andrew D.
REGISTRATION NUMBER: 34,6
                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: 81
TOPOLOGY: linear
APPLICATION NUMBER: US 0 FILING DATE: 21-FEB-1992
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Pred. No. 19;
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                                                                                                                                                                                                                                                                        RESULT 10
US-09-724-425-9/c
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US-09-724-426-9
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APPLICANT: Reed, John
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of BCL-2 Gene
FILE REFERENCE: 10412-024
                                                                                                                                                                                                                                  Sequence 9, Application US/09724425
Patent No. 6841541
                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local Similarity 88.2%;
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Patent No. 6414134
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Best Local Similarity
                                               APPLICANT: Reed, John C.
TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
FILE REFERENCE: 04040/1200990-US7
CURRENT APPLICATION NUMBER: US/09/724,425
CURRENT FILING DATE: 2000-11-28
FRIOR APPLICATION NUMBER: US 09/375,514
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: DNA
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PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/124,256
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 33
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Pred. No. 19;
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Pred. No.
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19;
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PRIOR APPLICATION NUMBER: US 07/840,716

APPLICATION NUMBER: US 07/288,692

1988-12-22 1992-02

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JS-09-724-425-9
 Query Match
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cent No. 5831066
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                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                      STRANDEDNESS:
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                                                                                                                                                                (408)
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                       DNA (genomic)
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88.2%;
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 83.3%; Score 15;
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Length 17;
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RESULT 13 US-09-724-426-8/c

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                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
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: Virginia
                                             Similarity
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AGAGGGUCGCACGCG 15
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                     DNA (genomic)
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                                                            Score 15;
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0;
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                                                            Length 17;
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RESULT 15
US-09-108-673A-25/c
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FILE REFERENCE: 04040/1200990-US7;
CURRENT APPLICATION NUMBER: US/09/724,425
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/375,514
PRIOR FILING DATE: 1999-08-17
PRIOR PRICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR FILING DATE: 1993-06-05
PRIOR FILING DATE: 1993-09-20
PRIOR FILING DATE: 1993-09-20
PRIOR FILING DATE: 1993-09-20
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                                                                                                         Sequence 25, Application US/09108673A Patent No. 6887906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6414134
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 8
LENGTH: 1
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GENERAL INFORMATION:

APPLICANT: Ching-Leou Teng and Greg Hardee
TITLE OF INVENTION: Compositions and Methods for the Delivery of
TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal
NUMBER OF SEQUENCES: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1988-12-22
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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Local Similarity 93.3%;
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FILING DATE: 1992-02-21
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Pred. No.
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PRIOR APPLICATION DATA;
APPLICATION NUMBER: 08/886,829
PILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: PAUL K. Legaard
REGISTRATION UNMBER: 38,534
REFERENCE/DOCKET NUMBER: 181S-31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPAX: (215) 568-3100
TELEPAX: (215) 568-349
INFORMATION POR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
LENGTH: 17 base pairs
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2432
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2432, App
Patent No. 6812339
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Best Local Similarity
ORGANISM: Human
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP STREET: One Liberty Place, 46th Floor
                                         ENGTH: 955
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MEDIUM TYPE: DISKETT
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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OPERATING SYSTEM:
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ZIP: 19103
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FILING DATE: July 1, 1998
CLASSIFICATION: 514
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93.3%;
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    Mismatches

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Pred. No. 1.9e+02
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GAGGGUCGCACGCGG 16

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; ORGANISM: Humar
US-09-949-016-2433
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                  Query Match
Best Local
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Best Local Similarity
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                                                                       ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                      ENERAL INFORMATION:
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ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          FILING DATE:
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                    Similarity
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93.3%; Pred. No. 1.8e+02;
Score 15; DB
Pred. No. 1.8e
1; Mismatches
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Pred. No.
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                                   DB 3; Length 2036
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Patent No. 6812
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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09-949-016-14174
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                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
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ITLE OF INVENTION: WITH HUMAN DIGENCY.
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                                                                              RGANISM: Human
                                   AME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICANT: VENTER, J. Craig et al.
LE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                   FILING DATE: 2000-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2134 GAGGGTCGCACGCGG 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 GAGGGTCGCACGCGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14174,
NFORMATION: n = A, T, C or G
                                                                                                                                                                                                  LING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGGUCGCACGCGG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                  2000-09-08
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Pred. No. 1
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RESULT 22
US-07-841-651-1/c
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/ Sequence 16537, Application US/09949016

/ Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(14587)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16537
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07841651 Patent No. 5410031
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/841,651
FILING DATE: 19920224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                         STREET: 4. STREET: 4. CITY: Pasadena CITY: California TICA
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                            ZIP: 91101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 83.3%; Score 15; DB 3;
Similarity 93.3%; Pred. No. 1.7e+02
14; Conservative 1; Mismatches
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                                                                                                                                                                                                                                         225 South Lake Avenue, Ninth Floor
                                                                                                                                                                                                                                                                                                                                                                                 Wright, Ernest M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%; Score 15; DB 3; llarity 93.3%; Pred. No. 1.8e+02; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                 Pajor, Ana M
                                                                                                                                                                                                                                                               Sheldon
                                                                                                                                                                                                                                                                                                                     Cloning and Functional Expression of a Mammalian Na+/Nucleoside Cotransporter: A Member SGLT Family
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                    US/07/841,651
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RESULT 23
US-08-311-731A-138/c
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNDEER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION UNDEER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                       TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2238 base not rever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS: 411
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mandel, SaraLynn
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SMITH, DOU APPLICANT: MAO, JEN-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: (818) 796-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: BOSTON
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                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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TOPOLOGY:
                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECULE TYPE:
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Pred. No. 3.6e+02;
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; OTHER INFORMATION: ; OTHER INFORMATION: US-09-952-060-31
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US-08-311-731A-138
                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FO
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                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION NUMBER: PCT/US01/28861
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                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-03-27
APPLICATION NUMBER: 60/233,180
FILING DATE: 2000-09-15
                                                                                                                                                                                 25690 AGAAGGTCGCACGCGG 25675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-09-14
APPLICATION NUMBER: 60/317,814
FILING DATE: 2001-09-07
APPLICATION NUMBER: 60/279,056
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                                                                 INFORMATION:
                                                                                                26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Casimiro, Danilo R.
INVENTION: ENHANCED FIRST GENERATION J
INVENTION: VACCINES EXPRESSING CODON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGAGGGUCGCACGCGG 16

    Application US/09952060
6733993

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Chen, Ling
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             Bett, Andrew J.
                                Youil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: US/09/952,060
NG DATE: 2001-09-14
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Burg
                                              Emilio A.
                                                                                                                                                                                                                                                                                                                                Codon optimized DNA encoding pMRKAd5HIV-1 nef, noncoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODIFICATIONS
                                                                                                                                                                                                                                                              80.0%;
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Pred. No. 3
                                                                                                                                                                                                                                                              Score 14.4;
Pred. No. 3
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US-09-952-060-26
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                                                                                               SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
                                                                                                                                      NUMBER OF SEQ
                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
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                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/952,060
                                                                                                                                                                                                                                                                          RIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIOR APPLICATION NUMBER: 60/233,180 RIOR FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: DNA encoding pMRKAd5 HIV-1 gag, noncoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: 'Casimiro, Danilo
OTHER INFORMATION:
                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
                                                                           ENGTH: 38519
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Local Similarity 87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/279,056 FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/
FILING DATE: 2001-09-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29, 233993
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                                                                                                                 FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaslow, David C.
                                                                                                                                      ID NOS:
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                                                                                                                   for Windows Version 4.0
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Codon optimized DNA encoding pMRKAd5HIV-1 pol,
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Pred. No. 3.
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US-09-949-016-12147/c
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                    SEQ ID NO 17361
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17361, App
Patent No. 6812339
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Best Local :
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SEQ ID NO 12147
LENGTH: 767677
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APPLICANT: VENTER, J.
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Patent No. 6812339
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Best Local
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE REFERENCE: CLOU307
                                                                                                                                            PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                         SOFTWARE: FastSEQ for Windows Version
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERSOF
FILE REFERENCE: CL001307
                                                                TYPE: DNA
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FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(767677)
OCHER INFORMATION: n = A,T,C or
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NAME/KEY: misc_feature
                                           ORGANISM: Human
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1 Similarity 93.8%;
15; Conservative
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Pred. No. 3.5e
1; Mismatches
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Pred. No. 3.1e+02;
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3.5e+02;
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361
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Best Local S
Matches 13
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APPLICANT: FLBISCHMAN, Robert
APPLICANT: WHITE, Owen R.
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                                                                                                                                              SEQ ID NO 2
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Patent No. 6294328
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                                                                                                                                                             TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.1
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FEATURE:
OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: 1
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                     TYPE: DNA
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                                                                           ORGANISM: Mycobacterium tuberculosis
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Local Similarity 81.2%;
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Local Similarity 93.8%;
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FRASER, Claire M.
VENTER, John C.
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"n" bases at various positions throughout the sequence represent a, t, c or \boldsymbol{g}
                                        CDC 1551
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Pred. No. 2.2e+02;
2; Mismatches 1,
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Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: FLEISCHMAN, Robert D.
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                                                                                                                           ORGANISM: Mycobacterium tuberculosis
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CACGCGGTA 991723
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Pred. No. 2.2e
1; Mismatches
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Pred. No. 2
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Pred. No. 2
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MOLECULE TYPE:
ANTI-SENSE: YE
                                                                                                                        ent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/288,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
IOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILING DATE:
                                                                                                                                        10,
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                                                                                                                                                                                                                                                                                Similarity
12; Conserv
                                                                                                                                                                                                                                                  5 GGUCGCACGCGGUA 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08465485A
                                                                                                                                            Application US/09080285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: P.C.
1755 S. Jefferson Davis Hwy.,
: P.C.
1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (408)
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                                                                                                                                                                                                                                                                                                                                                               YES
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                                OBLON, SPIVAK, McCLELLAND, MAIBR & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-SEP-1993
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                                                                                                John
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                                                                              Regulation of bcl-2 Gene Expression
                                                                                                                                                                                                                                                                                                 77.8%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 07/840,716
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                                                                                                                                                                                                                                                                                                              Length 17
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APPLICANT: Reed, John
ITIES OF INVENTION: Regulation of BCL-2 Gene Expression
FILE REFERENCE: 10412-024
CURRENT APPLICATION NUMBER: US/09/724,426
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                RESULT 35
US-09-724-426-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-080-285-10
   Best Local Similarity 85. Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09724426
Patent No. 6414134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                       Query Match
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                                                                             -09-724-426-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840
FILING DATE: 21-FEB-1992
PRIOR APPLICATION NUMBER: US 07/288
PILING DATE: 22-DEC-1988
PILING DATE: 22-DEC-1988
ATTORNEY, AGENT INFORMATION:

NAME: FORTHEY, Andrew D.

REFERENCE/DOCKET NUMBER: 33,600
REFERENCE/DOCKET NUMBER: 3355
TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (408) 436-2075 INFORMATION FOR SEQ ID NO: :
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APPLICATION NUMBER: US 01
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM: PC-DOS/MS-DOS
SOUTWARE: PAt-entin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: |
ANTI-SENSE: YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Ar
STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 20-SEP-1993
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: Virginia
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77.8%; Score 14; DB 3; Length 17; 85.7%; Pred. No. 6.2e+02; ative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.8%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 3;
Pred. No. 6.2e+02;
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 Gaps
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-425-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/465,485
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR FILING DATE: 1993-09-20
PRIOR APPLICATION NUMBER: US 07/840,716
PRIOR FILING DATE: 1992-02-21
PRIOR APPLICATION NUMBER: US 07/288,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09108673A Patent No. 6887906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 17
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Patent No. 6841541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                               SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/1
FILING DATE: July 1, 1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION FILE REFERENCE: 04040/1200990-US7 CURRENT PELLICATION NUMBER: US/09/724,425 CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19103
ZIP: READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/375,514 PRIOR FILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/080,285
PRIOR FILING DATE: 1998-05-18
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6887906ris LLP
STREET: One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ching-Leou Teng and Greg Hardee
TITLE OF INVENTION: Compositions and Methods for the Delivery
TITLE OF INVENTION: Oligonucleotides Via the Alimentary Canal
NUMBER OF SEQUENCES: 132
APPLICATION NUMBER: 08/886,829
FILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   STREET: One Liberty CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                       STATE:
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85.7%;
                                                                                                                                      US/09/108,673A
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Pred. No. 6.2e+02;
2; Mismatches (
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ELECOMMUNICATION INFORMATION:

ELEPHONE:

568-

3100

SIS-3105

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JS-09-108-673A-27/c
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                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/886,829
PILING DATE: 01-JUL-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: (
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                            REFERENCE/DOCKET NUMBER: IS LECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION DATE:
   STRANDEDNESS:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/108,673A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 85.
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Philadelphia
               Nucleic Acid
                                                                                                                                                           Paul K. Legaard
                                                                                                                                                                                                                                                                                                                                                                                                                     PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        one
                              17 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                              (215)
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                                                                                                                                                                                                                                                         July 1, 1998
                                                                                                                                                                                                                                                                                                                                                     DISKETTE, 3.5 INCH, 1.44 MB STORAGE
Single
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Oligonucleotides Via the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-1995
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                                                                                                                                           38,534
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Pred. No. 6.2e
2; Mismatches
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Alimentary Canal
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-- 'ocal Similarity
                                                                 Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                             Sequence 20854, Application US/09270767
Patent No. 6703491
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                                                                                                                                                                                                                                                      APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                 09-270-767-20854/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Drosophila melanogaster
                                                                                                                                                DRGANISM: Drosophila melanogaster
                                                                                                                                                                                      ENGTH: 397
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                                                                                                                                                                      DNA
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                                                                                 Similarity
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Similarity 92.9%;
                              GAGGGUCGCACGCG 15
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20-SEP-1994
                                                                               77.8%;
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85.7%;
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Pred. No. 6.2e
2; Mismatches
                                                                                   Score 14;
Pred. No.
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Application US/09676519

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RESULT 43
US-09-270-767-7758
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; ORGANISM: Staphylococcus bacteriophage
US-09-676-519-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-019-455A-15/c
                                     Sequence 7758, Application US/09270767 Patent No. 6703491 GENERAL INFORMATION:
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SEQ ID NO 15
LENGTH: 24
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Best Local Similarity
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Best Local Similarity
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APPLICANT: OHKUBO, SHOICHI
APPLICANT: MOGI, SHINICHI
APPLICANT: MOGICHI, YUKO
TITLE OF INVENTION: NOVEL PEPTIDE AND DNA THEREOF
FILE REFERENCE: 56804-46342
CURRENT APPLICATION NUMBER: US/10/019,455A
CURRENT FILING DATE: 2002-04-22
RUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: DUBOW, MICHAEL
TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BATERIOPHAGES
TITLE OF INVENTION: JA, 77, AND 96 THAT ENCODE ANTI-MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0404
CURRENT APPLICATION NUMBER: US/09/676,519
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 09/407,804
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 36
SOFTMARE: Patentin Ver: 2.1
 APPLICANT: Homburger et al. TITLE OF INVENTION: Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ITOH, YASUAKI
APPLICANT: NISHI, KAZUNKI
APPLICANT: OGI, KAZUHIRK
APPLICANT: OHKUBO, SHOIL
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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92.9%;
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82.4%; Pred. No. 7.8
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Pred. No. 5.5e
1; Mismatches
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of Drosophila melanogaster
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US-09-270-767-23040
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                                                                                                                                                        Sequence 2747, Application US/09513999C
Patent No. 6783961
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
PITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILLE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US/09/513,999C
                                                    PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOPTWARE: Patent.pm
SEQ ID NO 2747
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CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 23040
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CURRENT FILING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7758
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Best Local S
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Best Local Similarity
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                       TYPE: DNA
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ORGANISM: Homo sapiens
                                          ENGTH: 364
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Pred. No. 7.5e+02
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NAME/KEY: CDS LOCATION: 27..362

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US-09-513-999C-2747
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                                                                                                                                                                                      SEQ ID NO 10334
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                                                            Matches
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Patent No. 6703491
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-09-270-767-25712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-270-767-25712/c
                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                    LENGTH: 600
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                              1 AGAGGGUCGCACGCGGU 17
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AGTGGGTCGAACGCGGT 212
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76.5%;
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Pred. No. 7
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RESULT 48 US-09-949-016-150767/c

Myxococcus xanthus Genome Sequences and Uses Thereof

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US-09-252-991A-8441
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NUMBER OF SEQ ID NOS:
SEQ ID NO 8441
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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CURRENT FILING DATE: 1999-02-18
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ORGANISM: Human
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ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS
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Abd16350 Pseudomon
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Aak64938 Human mus
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                                                                                                                   25-SEP-1999;
27-SEP-1999;
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                                                                                                         23-AUG-2000;
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AAV88562
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Ac121997 DNA clone
Ac121996 DNA clone
Abd11974 Pseudomon
Adt46051 Bacterial
Ac121992 DNA clone
Abd07359 Pseudomon
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Ade77004 Human cDN
Aah28816 Drosophil
Aca23424 Prokaryot
Ac221976 DNA clone
Ac121977 DNA clone
Ac4270322 Human cDN
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Ac121983 DNA clone
Ass91654 DNA encod
Abz08504 Human leu
Ac122000 DNA clone
Ac121999 DNA clone
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Abs61473 Prostate
Acl59924 Human col
Acl66578 M. xanthu
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Rice a
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Vaccinating against tumors, infectionsing immunostimulatory Py-rich and

infectious diseases, allergies and rich and TG nucleic acids.

asthma

The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject

Claim

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Page

26;

276pp; English.

Inhibiting angiogenesis in a subject, antiangiogenic nucleic acid molecule (

6

the

subject.

involves administering

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least

one

WPI; 2001-273485/28

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RESULT 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy; retinopathy of prematurity; macular degeneration; corneal graft rejection; neovascular glaucoma; retrolental fibroplasia; rubeosis; Osler-Webber Syndrome; myocardial angiogenesis; plaque neovascularisation; telangiectasia; haemophiliac joint; angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     against tumour antigens, viral antigens (e.g. herpesviridae, retrovirid and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method also useful for preventing cancer, asthma, infectious disease, allergy immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acid can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth; tumour metastasis; precancerous lesion; rheumatoid arthritts;
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                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                   WO200253141-A2
                                                                                                                                                                                                                                                       14-DEC-2000; 2000US-0255534P
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RESULT 3
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Best Local Similarity
                                                                                                                                                                                                                    The present invention relates to methods for treating or preventing cancer, involving administering to a subject having or at risk of developing cancer immunostimulatory nucleic acids that induce expression of cell surface antigens and antibodies. The methods are useful for treating or preventing cancer such as basal cell carcinoma, bladder
                                                                                       cancer, bone cancer, brain and central nervous system (CNS) cancer, breast cancer, cervical cancer, colon and rectum cancer, connective tissue cancer, osophageal cancer, eye cancer, kidney cancer, laryn: cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, nelanoma, myeloma, oral cavity cancer, ovarian
                                              cancer, stomach cancer,
                                                                 cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 112; 312pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or preventing cancer, such as basal cell carcinoma, administering immunostimulatory nucleic acids that induce exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2000; 2000US-0213346P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-US020154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL38704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL38704 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IOWA ) UNIV IOWA RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunostimulatory nucleic acid SEQ ID NO: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neovascularisation, telangiectasia, haem wound granulation, intestinal adhesions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypertrophic scars.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rubeosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface antigens and antibodies to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTACAGCCAGGACTACGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osler-Webber Syndrome, myocardial angiogenesis, plaque arisation, telangiectasia, haemophiliac joints, angiofibroma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartmann
                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastasis; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ဂ္
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                immunostimulatory oligonucleotide described in the
                                              testicular cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            acids that induce expression of a subject having or at risk of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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ADB36764 ID ADB: XX

ADB36764 standard; DNA; 20

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RESULT 5

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Best

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Pred. No. 9.3 2; Mismatches

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AGGUACAGCCAGGACUACGA 20

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   Query Match
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                                                                                                           The invention describes a method of treating non-allergic inflammatory disease comprising administering to a subject having or at risk of developing a non-allergic inflammatory disease an immunostimulatory nucleic acid for prevention or treatment of the disease. The method is useful for treating non-allergic inflammatory diseases, such as
                                Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                             psoriasis, eczema, allergic contact dermatitis, latex dermatitis or inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease. This sequence represents an immunostimulatory nucleic acid
                                                                                                                                                                                                                                           Treating non-allergic inflammatory diseases, such as psoriasis, allergic contact dermatitis, latex dermatitis or inflammatory b disease by administering an immunostimulatory nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiulcer; gene therapy; vaccine; non-allergic psoriasis; eczema; allergic contact dermatitis; inflammatory bowel disease; ulcerative colitis;
                                                                                                                                                                                                                 Disclosure; Page 19; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                 Krieg AM, Berg DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003050268-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                  WPI; 2003-521815/49
                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAR-2001; 2001US-0279642P
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2002; 2002US-00112653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACD99693 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulatory nucleic acid #379.
                                                                                                                                                                                                                                                                                                                                                                                                  (KRIB/)
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                                                                                                                                                                                                                                                                                                                                                                                 KRIEG A M.
BERG D J.
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100.0%;
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 Score 20;
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DB 9; Length 20;
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                                                                                                                                                                                                                                                                                                                                               Query Match
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hypo-responsive subject; immunostimulatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method of treating or preventing allergy or asthma which comprises administering to a subject a poly-G nucleic acid in an aerosol formulation. The methods and compositions of the present invention are useful for diagnosing and/or treating asthma and allergy especially in a hypo-responsive subject. The present sequence represent an immunostimulatory nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bratzler RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-2000; 2000US-0179991P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating and/or preventing allergy or asthma using an immunostimulatory nucleic acid alone or in combination with an asthma/allergy medicament.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                 ss; antiasthmatic; antiallergic; dermatological; antiinflammatory; antibacterial; virucide; immunoglobulin E antagonist; allergy; immunostimulator; asthma; rhinitis; urticaria; dermatitis; bacterial infection; viral infection.
                                                                                                                                                      Allergic response suppressor oligonucleotide #391.
                                                                                                                                                                                                     ADU89707;
                                                                                                                                                                                                                          ADU89707 standard;
                                                                                                                                                                               10-FEB-2005
                                                        US2004235774-A1
                                                                             Synthetic
            23-APR-2004; 2004US-00831778.
                                  25-NOV-2004
                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) BRATZLER R L.
) PETERSEN D M.
) FOURON Y.
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                                                                                                                                                                                                                                                                                                                                                                       BP; 7 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 9.
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of suppressing a symptom of an allergic response in a subject by administering a first and second dose of an immunostimulatory nucleic acid that comprises a nucleotide sequence comprising 5'-cg-3', and where the second dose is administered from 1 day to 8 weeks after the first dose. The methods and compositions of the present invention are useful for the treatment or prevention of asthma and allergy, including rhinitis, urticaria and atopic dermatitis, using an immunostimulatory nucleic acid alone or in combination with other medicaments. They can also be used in preventing bacterial and viral infections. This sequence represents an oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suppressing allergies, including asthma, rhinitis, urticaria and atopic dermatitis, in a subject, comprises administering a first and second dos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-833006/82.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BRAT/) BRATZLER R L. (PETE/) PETERSEN D M. (FOUR/) POURON Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-0179991P.
02-FEB-2001; 2001US-00776479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                        11-MAY-1993;
20-JAN-1995;
18-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immune modulation; immune stimulation; bacterial infection; infendotoxic shock; antibacterial; antimicrobial; immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADW79936 standard; RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial
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                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                        29-OCT-1996;
17-NOV-1998;
                                                                                                                                                                                                                                10-FEB-2005.
                                                                                                                                                                                                                                                                                  US2005032731-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunostimulant; adjuvant; ss.
                                                                                                                                                                             15-MAR-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunostimulatory nucleic acid.
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18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulatory CpG oligoribonucleotide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
93US-00059745.
95US-00376175.
95US-00517016.
96US-00739264.
98US-00193653.
2001US-00883550.
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                                                                                                                                                                                2004US-00800926
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        /*tag=  a
/note= "CpG dinucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 5 C; 6 G; 2 T; 0 U; 0 Other;
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Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
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WPI; 2005-161694/17

(MARS/) MARSHALL W

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RESULT 8
AET40830
ID AET4
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AET40830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            daapted a non-toxic alerting response to their release from bacteria. The circumstant also relates to a method for the preparation of the bacterial of the by subjecting bacteria to one or more periods of stress, separating the ORNs and media from the bacteria, and filtering the separated product to remove substances with a molecular weight of more that 10 kD; and a comethod of using the filtrate to modulate/stimulate the immune system of animal to withstand microbial infection. The composition and methods of the invention are useful for modulating and/or stimulating the immune consistent of animals (including humans, poultry and livestock), particularly to withstand microbial infections or the onset of endotoxic shock. The compositions may be administered orally (e.g., as a food supplement) or compositions may be administered as an adjuvant for oral or compositions may also be administered as an adjuvant for oral or compositions may additionally be used to extend the viability of monocytes, thereby improving their composition contains on the onset of endotoxic abook. The composition and may be used to destroying normal T-cells in people with HIV infections. The composition of the invention contains or or fight infections. The composition of the invention contains or or such that in factions and may be used to contain the invention contains or or such that in people with HIV infections. The composition of the invention contains or or such that in people with HIV infections. The composition contains or or such that in people with HIV infections or pathogenic containing them are non-toxic. The present sequence compositions are people with HIV infections. The compositions becomes the manual compositions because of the invention contains or or such contains or pathogenic containing them are non-toxic. The present sequence compositions the manual compositions contains or pathogenic contains or pathogenic
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                                                                                                                                                      Toxic effect; gene expression profile; renal toxicity; toxicity marker; database; drug screening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABT40830
                                                                      Rattus norvegicus.
                                                                                                                                                                                                                                                                          Toxicity modelling related rat
                                                                                                                                                                                                                                                                                                                                                          26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABT40830 standard; DNA; 5253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing them are non-toxic. The present sequence represents a specifically claimed bacterial CpG oligoribonucleotide present in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition for modulating and/or stimulating immune system of animal useful for withstanding microbial infections and lethality of endotoxic shock, comprises low molecular weight oligoribonucleotide from bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                 screening; toxicity assay; rat; ds
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                                                                                                                                                                                                                                                                      gene SEQ ID No
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WO200295000-A2

ADV39876 ID ADV: XX RESULT 9

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ADV39876 standard; cDNA; 5253 BP

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                                                                                                                                                                            The invention relates to a novel method of predicting at least one toxic conference of a compound. The method comprises a gene expression profile of a compound, and comparing the gene conference or cell sample exposed to the compound, and comparing the gene conference or cell sample exposed to the compound, and comparing the gene conformation profile to a database compound, and townering the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the renal conformation of a toxic effect of a compound, predicting the renal conformation of a toxic effect of a predicting the renal conformation of a toxic effect of a compound, predicting the renal conformation of a toxic effect of a compound, predicting the renal conformation of a toxic effect of a compound, predicting the renal conformation or and toxic. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polymucleotide physiological states, or disease progression. This polymucleotide compounds are the specification. NOTE: The sequence data for this patent conformation format directly from the World Intellectual Property
                                                                                Best
                                                                  Matches
                                                                                                Query Match
                                                                                                                                Sequence 5253 BP; 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JUL-2001
10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          profile to a database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-148464/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-2002;
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19-JUN-2001;
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                                                                                  Local
                               2 GGUACAGCCAGGACUACG 19
                                                                                  Similarity
GGTACAGCCAGGACTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002US-0372794P
2002US-0371679P
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2002US-0357842P
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2001US-0330462P.
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2001US-0315047P.
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                                                                               90.0%;
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                                                                               Score 18;
Pred. No.
                                                                  Mismatches
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                                                                                1.2e+02;
                                                                                                  DB 10;
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                                                                                                Length 5253;
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                                                             Gaps
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2679 GGTACAGCCAGGACTACG 2696

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cc tachycardia, myocardial ischemia, angina, hypertension, hypotension, cc tachycardia, myocardial ischemia, angina, hypertension, hypotension, cc dyspnea, cardiogenic shock or other specific heart pathologies. The cc invention is based on the elucidation of globbal changes in gene cc expression in tissues or cells exposed to known toxins, particularly cc markers) that are differentially expressed on toxin exposure. The cc invention also relates to methods for predicting the progression of a cc compound's toxic effects, for predicting the cardiotoxicity of a cc compound, for identifying an agent that modulates the onset or cc progression of a toxic response, and for predicting which cellular progression of a toxic response, and for predicting which cellular cc progression of a teast two hybridization probes specific for toxicity prediction genes, and solid supports and kits comprising the concity predicting the toxic effects (especially cardiotoxic effects) of compounds such as pharmaceutical agents or environmental pollutants. Sequences ADV39135-ADV41830 represent cardiotoxic effects) of compounds such as pharmaceutical agents or environmental pollutants. Sequences ADV39135-ADV41830 represent cardiotoxicity marker sequences of rat origin whose expression is altered on exposure to polynucleotides of rat origin whose expression is altered on exposure to form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic compounds.
Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toxicology screening; drug screening; cardiotoxicity, drug-induced; expression profile; gene expression; myocarditis; heart arrhythmia; tachycardia; myocardial ischemia; angina; hypertension; hypotension; dyspnea; cardiogenic shock; cardiovascular disease; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat cardiotoxicity marker gene, SEQ ID NO:742
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Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a compound by obtaining a gene expression profile of a tissue or cell sample exposed to the compound and comparing the gene expression profile to a database of toxicity prediction genes which are differentially expressed on exposure to known toxins. The tissue or cell sample is preferably derived from heart tissue, and the predicted toxic effect is especially a cardiotoxic effect such as myocarditis, arrhythmias,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting a toxic effect of a compound by obtaining a gene expression profile of a tissue or cell sample exposed to the compound and comparing the gene expression profile to a database comprising all of the data given in the specification.
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DDBJ; AB012214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 742; 520pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of predicting at least one toxic effect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) GENE LOGIC INC
                                                               Sequence
Local Similarity
                                                                   5253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                 BP;
                                                                 1380 A; 1379 C; 1440 G; 1054 T; 0 U; 0 Other;
  90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson KR,
  Score 18; DB 13;
Pred. No. 1.2e+02;
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                           DB 13;
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                           Length 5253;
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GGUACAGCCAGGACUACG 19

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Mismatches

Indels

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Gaps

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124 AAGGACAGCCAGGACTACGA 143

0

Matches

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RESULT 10
RAZ50957
ID AAZ50957
AXX AAZ50
XX AAZ50
XX AAZ50
XX AAZ50
XX DESCRIPTION OS PSEU
XX WO20
XX ILLXI
FT CDS
                                                                                                                                                                                                                                            The patent discloses a method of initiating transcription of a target CC gene in a eukaryotic cell, by applying a chemical inducer capable of CC binding to the response protein produced by the eukaryotic cell itself, CC to form an inducing complex which binds to and induces the inducble CC promoter operably linked to the target gene. The gene switch is useful CC for externally regulating the target gene expression. This method is CC useful for selectively controlling peets in the fields, in gene therapy CC and to produce transgenic plants like melons, mangoes and soybean. It can be used to switch on genes which produce lethal proteins, that can be CC employed in the treatment of cancer. The present sequence is the Pseudomonas aeruginosa response regulator protein, lask encoding DNA. CC CLASK is a positive transcriptional activator, that responds to signals from the LasI inducer gene, that directs the synthesis of autoinducer, N-CC (3-oxododecanoly)-L-homoserine lactone (OdDHL)
S
                                                                      Matches
                                                                                                  Query Match
Best Local
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gene switch; pest control; gene therapy; transgenic plant; mango; melon;
soybean; lethal protein; treatment; cancer; LasR; OdDHL;
N-(3-oxododecanoly)-L-homoserine lactone; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ50957 standard; DNA; 720 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 74-75; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-224341/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinez A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing target gene expression in plants such as melons, mangoes, soybean, via a gene switch operably linked to a foreign gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY70035
                                                                                                                                                                                         Sequence 720 BP; 145 A; 200 C; 227 G;
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                                                                                                      Similarity
            AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB002653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Lask response regulator protein"
/note= "Induced by autoinducer, N-(3-oxododecanoly) -L-
homoserine lactone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                         84.0%;
85.0%;
                                                                            1; Mismatches
                                                                                                                                         Score 16.8;
                                                                                                            Pred. No.
                                                                                                                                                                                                     148 T; 0 U;
                                                                                                               4e+02;
                                                                                                                                         DB 3;
                                                                                  2;
                                                                                                                                            Length 720;
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RESULT 12
ABD33090
ID ABD33
XX
AC ABD33
XX
DT 18-NC
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                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                    of Pseudomonas species using biochip technology. Sequences ABD01397 ABD17967 represent P. aeruginosa polynucleotides of the invention. The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
               18-NOV-2004
                                                                                                                                                                                                                                                            Sequence 735 BP; 150 A; 203 C; 232 G;
                                                                                                                                                                                                                                                                                                                                                                                                        prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                            ABD33090;
                                                                      ABD33090 standard;
                                                                                                                                                                                                                                                                                                                                                             including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 7959; 455pp; English.
                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-615309/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-ЛП-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa polynucleotide #7959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2004
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                                                                                                                                                                                                                    Local
                                                                                                                                              139
                                                                                                                                                                                                        17;
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENOME
                                                                                                                                           AAGGACAGCCAGGACTACGA 158
                                                                                                                                                                        AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                     Conservative
               (first entry)
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98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-00252991.
                                                                      DNA; 145068
                                                                                                                                                                                                                   84.0%;
85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                   Score 16.8;
Pred. No. 4e
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                               did not form part
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                                                                                                                                                                                                                              DB 11;
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                                                                                                                                                                                                                              Length 735;
                                                                                                                                                                                                                                                              0 Other;
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                                                                                                                                                                                                    0
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                 sequences
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投資数器
                                             Murine cancer-associated
          Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
cytostatic.
                                           (CA) gene MD07-006.
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PN

WO2004058146-A2

SE 15-JUL-2004

15-DEC-2003; 2003WO-US040081

17-DEC-2002; 2002US-00322281

段数段

(SAGR-) SAGRES DISCOVERY INC

Morris DW, Malandro MS,

Novel human cancer associated protein encoded within open reading cancer associated gene, useful as targets for diagnosing cancer.

Disclosure; SEQ ID NO 33; 182pp; English.

FXSX

inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate and monitoring the effect of the articancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bloactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a murine CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates ftp.wipo.int/pub/published_pct_sequences

Sequence 145068 BP; 38358 A; 33586 C; 33004 G; 36708 T; 0 U; 3412 Other;

Query Match

Matches Best Local 17; Similarity AGGUACAGCCAGGACUACGA Conservative 85.0%; 84.0%; : Score 16.8; Pred. No. 5. 20 Mismatches .7e+02 Length 145068; 0, Gaps ç,

DB 13;

RESULT 13 AAF10633

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50545

AGGTACTGCCAGGACCACGA 50564

AAF10633 standard; cDNA; 246 BP

AAF10633

13-MAR-2001 (first entry)

Fusarium venenatum EST SEQ ID NO:3156.

Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum, Aspergillus niger; Aspergillus oryzae; Trichoderma reseat; identification; recombinat culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss. niger; recombination;

Fusarium venenatum.

WO200056762-A2

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RESULT 14
ADU54674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC global expression of genes from FF cells allows the production potential CC global expression of genes from FF cells allows the production potential CC of the microorganisms to be improved. New genes may be discovered, CC of the microorganisms to be improved. New genes may be discovered, CC gene copy number variation and stability can be monitored. The expression CC gene copy number variation and stability can be monitored. The expression CC gene copy number variation and stability can be monitored. The expression CC gene copy number variation and stability can be monitored. The expression CC gene copy number variation and stability can be monitored. The expression CC conditions, environmental stress, spore morphogenesis, recombination, CC conditions, environmental stress, spore morphogenesis, recombination, CC conditions, environmental stress, spore morphogenesis, recombination, CC conditions, environmental cor random cDNA clones including elimination of CC advantages over genomic or random cDNA clones including elimination of CC and organisation of the microarrays based on function of the gene CC and organisation of the microarrays based on function of the gene CC products to facilitate analysis of the results. AAR07478 to AAR11247 CC represents ESTs from CC ESTs from Appergillus oryzae; and AAR14879 to AAR11878 represents ESTs from CC Aspergillus oryzae; and AAR14879 to AAR15337 represents ESTs from CC Trichoderma reesei, which are all specifically claimed in the present
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 246 BP; 67 A; 55 C; 64 G;
                                                                                                                    Gene expression; biochip; microarray; hybridization; EST;
                                                                                                                                                                                                    10-FEB-2005
                                                                                                                                                            Fusarium venenatum CC1-3 EST, SEQ ID NO:3156.
                                                                                                                                                                                                                                                                                    ADU54674 standard; cDNA; 246
                   US2004229367-A1
                                                             Fusarium venenatum; CC1-3.
                                                                                                   expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                             3 GUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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GTACAACCAGGACTACGA 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NORDISK BIOTECH INC.
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                                                                                                                                                                                                      (first entry)
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CC expression of genes in a first filamentous fungal cells. The method CC same genes in one or more second filamentous fungal cells. The method CC involves differentially labeling nucleic acids from the first and second CC involves differentially labeling nucleic acids from the first and second CC fungal cells with filuorescent reporter dyes, and adding the mixture of CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled polynucleotides to a substrate containing an array CC fluorescently labeled nucleic acids set and by fluorescence; CC expression of genes in the fungal cells is determined by fluorescence; CC entitted when labeled nucleic acids from the second fungal cell hybridise. CC cells used in the method are chosen from Acremonium, Aspergillus, CC cells used in the method are chosen from Acremonium, Aspergillus, CC cells used in the method are chosen from Acremonium, Aspergillus, CC reported from Filamentous fungal cells, in order to improve the cells, protein CC invention is useful for monitoring the expression of a plurality of genes of filamentous fungal cells, in order to improve the cells, protein CC strain ATCC 20334) which is specifically claimed for use in the method of the printed specification, but was obtained in electronic format CC serials ausnto. GOV secuence human off compart off cells at a specifical secuence format collars. The production compart to file at the filamentous fungal cells, but was such organisms are used for the industrial collars.
                                                                                                                                                                                                  RESULT 15
ADZ92677
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monitoring differential expression of genes in a filamentous fungal cell relative to expression of the genes in second filamentous fungal cells, comprises using microarrays containing Fusarium venenatum expressed sequence tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
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22-MAR-2000; 2000US-00533559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 3156; 274pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 246 BP; 67 A; 55 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seqdata.uspto.gov/sequence.html?DocID=US20040222367
differential expression; gene expression; filamentous fungus; expressed sequence tag; EST; variation; microarray; ss.
                                                                                                                                                                                 ADZ92677 standard; cDNA; 246 BP
                                                         Fusarium venenatum expressed sequence tag cDNA SEQ ID NO 3156
                                                                                                   11-AUG-2005
                                                                                                                                            ADZ92677;
                                                                                                                                                                                                                                                                              3 GUACAGCCAGGACUACGA 20
|:|| |||||:|||
154 GTACAACCAGGACTACGA 171
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      82.0%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 13
Pred. No. 5.8e+02;
2; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; recombinant DNA construct; drought tolerance; heaticide tolerance; cold tolerance; heat tolerance; drought tolerance; heaticide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; glant growth regulator; glantcomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag (EST) of ADZ93898-ADZ96922, and examining the array under fluorescence excitation conditions. (M1) is useful for monitoring global expression of several genes from a filamentous fungal cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. In (M1), one spot on an array equals one gene or open reading frame, extensive follow-up characterization is unnecessary since sequence information is available and EST microarrays can be organized based on sequence of the invention. (Note: this sequence corresponds to an EST sequence of the invention but can be obtained in electronic form from the lighton web site sequence but the lighton web site sequence.
                                                                                                                                                            Plant full length insert polynucleotide segid 8343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to expression of the same genes in one or more second filamentous fungal cells, comprises adding fluorescence labeled nucleic acids isolated from the cells to a substrate containing an array of Aspergillus oryzae expressed sequence tag (EST) of ADZ93898-ADZ96922, and examining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring differential expression of genes in first filamentous fungal cell relative to that of genes in second fungal cells, comprises hybridizing fluorescence labeled nucleic acids from the cells to an arr
                     yeaser-unearment production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein contest.
                                                                                                                                                                                                                                                                    ADX13768 standard; cDNA; 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3156; 264pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusarium venenatum.
                                                                                                                                                                                                                                                                                                                                                             154
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                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                   GUACAGCCAGGACUACGA
                                                                                                                                                                                                                                                                                                                                                          GTACAACCAGGACTACGA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site seqdata.uspto.gov/sequence.html; Document
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 55 C; 64 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                        82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tags.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a method of monitoring (M1) genes in a first filamentous
                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4; I
Pred. No. 5.8e
2; Mismatches
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RESULT 17
ADA03035/c
ID ADA030
XX
AC ADA030
XX
AC ADA030
XX
DT 06-NOV
DX
XX
MOUSe
XX
KW MOUSe;
XW MOUSe;
XX
XX
XX
Gene;

(first

entry)

ADA03035 standard;

DNA; 31632 BP.

prostate; Mouse; murine; Mouse Rorc 06-NOV-2003 ADA03035;

lymphoma;

carcinoma associated; oncogene; carcinoma; homa; leukaemia; cytostatic; gene therapy; or

grug

cancer; breast; lrug screening;

carcinoma associated gene,

SEQ ID NO:1553.

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GATACAGCCAGGACTACG

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                                    Matches
                                                                 Query Match
                                                                                                                                       plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                             polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as
                                                                                                Sequence 1308
                                                                                                                                                                                                                                                                                                                                                               The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999;
05-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                mproving yield.
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   2 GGUACAGCCAGGACUACG
                                  . Similarity
15; Conserv
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SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 8343; 15pp; English.
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Έν
                                  Conservative
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2001US-00985678
                                                                                              BP; 376 A;
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                                               82.0%;
83.3%;
                                                                                              282 C;
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   19
                                2
                                                 Score 16.4;
Pred. No. 6.
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                                  Mismatches
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                                                                                             372 T; 0 U; 0 Other;
                                                 5e+02
                                                               DB 13;
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                                                              Length 1308;
                                  Indels
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                               Gaps
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The invention relates to recombinant carcinoma associated (CA) nucleic combinant carcinoma associated proteins (CAP) encoded by them. The CC recombinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC invention also encompasses expression vectors and host cells comprising a CC invention were identified using CC interest to the protein, and a biochip comprising CA mucleic acid or CC patched in the rect. The sequences of the invention were identified using concegnic retroviruses, which insert into the genome of the host organism CC arrandom. Many of these do not carry transduced host oncogenes or CC at random. Many of these do not carry transduced host oncogenes or CC direct consequence of the effects of proviral integration into host pathogenic trans-acting viral genes, meaning that cancer incidence is a protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as tissues. CA nucleic acids, proteins and antibodies are also useful as the sequence of the invention. Note: The complete sequence CA nucleic acid present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this sequence of the printed specification, but was obtained cft. The electronic format directly from WIPO at CC in electronic format directly from WIPO at
RESULT 18
ADA66319/c
ID ADA66
XX
AC ADA66
XX
DT 20-NC
XX
DT 20-NC
XX
MOUSS
XX
KW CARC
KW CCARC
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2002; 2002WO-US041414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003057146-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-587068/55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1553; 245pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31632 BP;
                                   carcinoma-associated gene; CA gene; Rorc gene; mCG15938 gene; BAT1 gene; Iqgap1 gene; IQGAP1 gene; Zpf29 gene; hCG2759 gene; KCnJ9 gene; KCNJ9 gene; Pp3cc gene; Pp93cC gene; mCG9110 gene; hCG27579 gene; cancer cell; Jymphatic cell; breast cell; prostate cell; epithelial cell; carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer; vaccine; carcinoma, lymphoma carcinoma; lymphatic cancer; breast cancer;
                                                                                                                                                                                                                                    20-NOV-2003
                                                                                                                                                                                                                                                                                                                    ADA66319 standard; DNA; 31632
                                                                                                                                                                                             Mouse Rorc
                                                                                                                                                                                                                                                                                                                                                                                                                             26940
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTACAGCCAGGGCTAC 26923
                        cancer; DNA vaccine; animal model;
                                                                                                                                                                                           gene genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                       (first entry)
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Pred. No. 8e+02;
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This invention relates to a novel recombinant carcinoma-associated (CA) compulsive acid comprising a fully defined genomic, mRNA or coding sequences of mouse Rorc gene or human RORC gene, mouse EQ15938 or human gene BAT1, compuse Tggapl gene or human IQGAP1 gene, mouse EQ15938 or human gene BAT1, compuse Tggapl gene or human IQGAP1 gene, mouse EQ15938 or human gene BAT1, compuse Iggapl gene or human KCNU9 gene, mouse Ppp3cc gene or human KCNU9 gene, mouse Ppp3cc gene or human EQ27579 gene, as given in the specification. CA genes are genes which are preferably expressed in CC cancer cells, preferably lymphatic, breast, prostate or epithelial cells. CC carcinoma-associated proteins (CAP) may have cytostatic activity and the carcinoma-associated proteins (CAP) may have cytostatic activity and the carcinoma-associated proteins (CAP) may have cytostatic activity and the carcinoma-associated proteins (CAP) may have cytostatic activity and the carcinoma-associated proteins the use of gene therapy or a seful for diagnosis and treatment of carcinomas, especially lymphoma carcinoma, breast cancer and prostate cancer. The CA genes may also be carcinoma, breast cancer and prostate cancer. The CA genes may also be considered to the mouse Rorc gene genomic DNA sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant carcinoma-associated nucleic acid, evaluating the effect of a candidate carcinoma drug,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-569168/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31632 BP;
                                                                                                                                                                                                                               04-DEC-2003
                                                                                                                                                                                                                                                                                            ADB72773 standard;
                          26-DEC-2001; 2001WO-US051291.
                                                                                                                                                                     mouse;
                                                                                                                                                                                                   Mouse Rorc
02-MAR-2001; 2001US-00798586
                                                            30-JAN-2003.
                                                                                          WO2003008583-A2
                                                                                                                       Mus sp
                                                                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      26940
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                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                     de;
                                                                                                                                                     ds; cytostatic;
neoplasm; adeno
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                                                                                                                                                                                                   gene.
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                                                                                                                                                        adenocarcinoma;
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                                                                                                                                                                                                                                                                                            DNA; 31632
                                                                                                                                                                                                                                 entry)
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83.3%;
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                                                                                                                                                                     gene therapy; vaccine; carcinoma; lymphomas;
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Pred. No. 8e+02;
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                                                                                                                                                           sarcoma; gene.
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RESULT 20
ADA02933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                      Claim 1; SEQ ID NO 1451; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                          Morris
                                                                                                                                                                      26-DEC-2001; 2001US-00035832
                                                                                                                                                                                            26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                    17-JUL-2003
                                                                                                                                                                                                                                         WO2003057146-A2
                                                                                                                                                                                                                                                              Mus sp
                                                                                                                                                                                                                                                                                                             Mouse; murine;
                                                                                                                                                                                                                                                                                                                                 Mouse Braf carcinoma associated gene,
                                                                                                                                                                                                                                                                                                                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                ADA02933;
                                                                                                                                                                                                                                                                                                                                                                                                       ADA02933 standard; DNA; 96599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2001; 2001US-00004113.

08-NOV-2001; 2001US-00052482.

30-NOV-2001; 2001US-00997722.

20-DEC-2001; 2001US-00034650.
                                                                                                                                                (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26940
                                                             recombinant nucleic acid encoding carcinoma associated protein, ful for preparing compositions for treating carcinomas.
                                                                                                  2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                               SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTACAGCCAGGGCTAC 26923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGUACAGCCAGGACUAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31632 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 601; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplasm,
                                                                                                                                                                                                                                                                                                 lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Engelhard
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                          carcinoma associated; oncogene; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7931 A; 8130 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                leukaemia; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          묫
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.4;
Pred. No. 8e
                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7983 G;
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:1451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Be+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                              gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7588 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                          cancer; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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The invention relates to recombinant carcinoma associated (CA) acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them

nucleic

The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic

gene therapy,

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New recombinant nucleic acid,

adenocarcinoma,

or

useful for treating carcinomas,

lymphomas,

SEQ neoplasm,

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2304pp;

English

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RESULT 21
ADB72671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogenic trans-acting vital years, meaning the direct consequence of the effects of proviral integration into host protooncogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acide, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence represents a specifically claimed murine CA nucleic acid semience of the invention. Note: The complete sequence data for this
                                                                                                                                                                                                                                                     02-MAR-2001; 2001US-00798586
23-OCT-2001; 2001US-00004113
08-NOV-2001; 2001US-00052482
30-NOV-2001; 2001US-00997722
20-DBC-2001; 2001US-00034650
                                                                                                                                                           WPI; 2003-239337/23
                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a specifically claimed murine CA sequence of the invention. Note: The complete sequence data patent did not form part of the printed specification, but win electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse Braf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA nucleic acid, a polypeptide (especially an antibody) that sphinds to the protein, and a biochip comprising CA nucleic acid fragments thereof. The sequences of the invention were identif.
                                                                                                                                                                                                                                                                                                                                                      26-DEC-2001; 2001WO-US051291
                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003008583-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB72671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB72671 standard; DNA; 96599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 96599 BP; 28457 A; 18209 C; 18968 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenic trans-acting viral genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogenic retroviruses, which insert into the genome of the host of at random. Many of these do not carry transduced host oncogenes or
                                                                                                                                                                                                                        (SAGR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention also encompasses expression vectors and host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28454 AGGTACAGCCAGGGCTAC 28471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                          SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGUACAGCCAGGACUAC
                                                                                                                                                                                          Engelhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.4; DB 9;
Pred. No. 8.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30477 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identified using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ç;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 22
ADC85413
ID ADC85413
ADC86413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ś
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Best Local :
                                                                                                            Matches
                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 96599 BP; 28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;
                                                                                                                                                                                                                                                                         nucleotide sequence selected from any of the fully defined carcinoma-
associated (CA) genes from the 50 tables given in the specification. The
CA proteins are secreted, transmembrane or intracellular proteins. The
recombinant nucleic acids are useful for screening for drug candidates
for diagnosing or treating carcinomas. Sequences given in ADC85215-
ADC85514 represent CA genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; secreted; transmembrane; intracellular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Braf genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC85413;
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcin associated (CA) genes from the 50 tables given in the specificat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC85413 standard; DNA; 96599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-2002; 2002WO-US038582.
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-513603/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28454 AGGTACAGCCAGGGCTAC 28471
28454
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                                                                                                            l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                    ۳
                                                                                                                                                                                                                              96599 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 199; 983pp; English.
AGGTACAGCCAGGGCTAC 28471
                                                       AGGUACAGCCAGGACUAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                               Conservative
                                                                                                                                                                                                                        28457 A; 18209 C; 18968 G; 30477 T; 0 U; 488 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%;
83.3%;
                                                                                                                                         82.0%;
83.3%;
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Pred. No. 8.6e+02;
                                                       18
                                                                                                               <u>ب</u>
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                                                                                                                                            Score 16.4; DB 10
Pred. No. 8.6e+02;
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                                                                                                                    Mismatches
                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 96599;
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                                                                                                                                                                      Length 96599;
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                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          The
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ADM74528 ID ADM7 XX

ADM74528 standard; DNA; 96599 BP

Query Match
Best Local Similarity 83.3
Conservative

2;

Mismatches

Score 16.4; DB 12 Pred. No. 8.6e+02;

DB 12;

Length 96599; Indels

<u>.</u>

Gaps

0

Sequence 96599

BP;

28457 A; 82.0%; 83.3%;

18209 C; 18968 G; 30477 T; 0 U; 488 Other;

seqdata.uspto.gov/sequence.html.

RESULT 23

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CC also relates to a host cell comprising a recombinant nucleic acids. The invention compression vector, an expression vector comprising a recombinant nucleic acid or carcinoma associated protein, a method of screening for drug candidates, a cc carcinoma associated protein (CAP) encoded by a nucleotide sequence, a cc carcinoma associated protein (CAP) encoded by a nucleotide sequence, a cc carcinoma drug, a method of diagnosing carcinoma, a method of carcinoma, a method of carcinoma, a method of evaluating the effect of a candidate cc carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting the estivity of a CAP, a method of evaluating the effect of a candidate cc carcinoma drug, a method of evaluating the drug to a patient, removing a cell sample from the patient and determining alterations in the cappression or activation of a gene comprising the nucleotide sequence. A cc expression or activation of a gene comprises determining the expression of a second normal tissue type from the first individual and comparing the expression indicates that the first individual and comparing the expression indicates that the first individual and comparing the expression indicates that the first individual and comparing the expression indicates that the first individual and comparing the expression indicates that the first individual and comparing the expression indicates carcinoma. A method of inhibiting the cappression of the gene from the CAP. The CAP. Treating carcinoma a patient an inhibitor of CAP. Comparises administering to a patient an inhibitor of CAP. Comparises administering to a patient an inhibitor of CAP. Treating carcinoma comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for preparing a composition for diagnosing or treating carcinoma e.g., comparing a patient and carcinoma e.g., comparing a composition for diagnosing or treating carcinoma e.g., comparing a composition of the protein encoded by the comparing carcinoma carcin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; carcinoma associated nucleic acid; CA nucleic acid; carcinoma; leukaemia; l)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine carcinoma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2004
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02-MAR-2001; 2001US-00798586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MORR/) MORRIS D W. (ENGE/) ENGELHARD E
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lymphoma;
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RESULT 25
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Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABL1675) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the
Drosophila melanogaster expressed polynucleotide SEQ ID NO 24191.
                         26-MAR-2002
                                                ABL09903;
                                                                    ABL09903 standard; cDNA;
                                                                                                                                                                                                                        Sequence 2550 BP;
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genes from Drosophila and
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11-JUL-2000;
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2000US-00614150.
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                                                                                                                                                                                                                                                      e data for this patent did not form part of the but was obtained in electronic format directly
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11-JUL-2000; 2000US-00614150
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23-MAR-2001; 2001WO-US009231
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                                                                                                   WO200171042-A2
                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                 pharmaceutical; gene; ds.
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genes from Drosophila and
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11-JUL-2000; 2000US-00614150
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from WIPO at ftp.wipo.int/pub/published_pct_sequences
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P-PSDB; ABB65800.
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Similarity 87.5%;
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RESULT 27
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genes from Drosophila and
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                                                        New isolated nucleic acid genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                   pharmaceutical; gene;
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                        Claim 1; SEQ ID NO 24188;
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                biology; cell signalling; insecticide
                                                           detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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isolated nucleic acid detection reagent

21pp + Sequence Listing;

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39970 GTÁCAGCCAGGÁCTAC 39985

GUACAGCCAGGACUAC

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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ97596;
                                                                                                                                                      The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-DEC-2002; 2002US-00330773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-2003; 2003WO-US041389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004060304-A2
                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 573; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morris DW,
                                                                                                         Sequence 90616 BP; 22442 A; 19414 C; 20208 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus.
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                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
                               80.0%;
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Pred. No.
                                  Score 16; DB 12;
Pred. No. 1.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Le..
. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma; Mouse;
                                                                                                                    27923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4989
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                                                           Length 90616;
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-
                                              Mus sp.
                                                                               Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                   Mouse Sos1 carcinoma associated gene, SEQ ID NO:1337
                                                                                                                                             06-NOV-2003
                                                                                                                                                                       ADA02819;
                                                                                                                                                                                            ADA02819 standard; DNA; 96600 BP
                                                                                                                                                                                                                                                                                                                                                           Sequence 96599 BP; 27390 A; 19000 C; 20559 G; 29350 T; 0 U; 300 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 84; 983pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant nucleic acid comprising a nucleotide sequence of any the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-513603/48
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                      WO2003057146-A2
                                                                      gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Egr2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; gene therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                   represent CA genes of the invention.
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                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; carcinoma-associated gene; CA;
                                                                                                                                                                                                                                                                                                                       1.3e+03;
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02-MAR-2001; 2001US-00798586 23-OCT-2001; 2001US-00004113

26-DEC-2001; 2001WO-US051291

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WO2003008583-A2

¥ \$ \$ \$

Mus sp.

mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.

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Mouse Sos1 gene.

04-DEC-2003

(first entry)

ADB72557;

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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (AAAA01482-AAA03094), and to CC recombinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CCA nucleic acid, a polypeptide (especially an antibody) that specifically CC binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct consequence of the effects of proviral integration into host CC protoconcogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence CC issues. CA nucleic acids, proteins and antibodies are also useful as CC therapeutic agents and in screening and evaluating drug candidates. The present sequence of the invention. Note: The complete sequence CA nucleic acid consequence of the invention. Note: The complete sequence can and on this description but was obtained consequence of the invention. Note: The complete sequence has not a brained consequence of the invention. Note: The complete sequence was obtained.
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                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
ADB72557 standard;
                                                                                                                                                                                                                                                                                                                              Sequence 96600 BP; 27391 A; 19001 C; 20558 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-587068/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1337; 245pp; English.
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                                                                                                                                                                                                                                                        Local
                                                                                                                          91766 GTÁCAGCCAGGACTÁC 91781
                                                                                                                                                                            3 GUACAGCCAGGACUAC 18
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                Conservative
DNA;
                                                                                                                                                                                                                                                     80.0%;
96600 BP
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                                                                                                                                                                                                                                                     Score 16; DB 9;
Pred. No. 1.3e+03
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RESULT 32
ADM74414
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Best Local (
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30-NOV-2001;
20-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAGR-) SAGRES DISCOVERY.
                                                                                                                                                                                                                                                                                                                             Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                   Murine
                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                  ADM74414;
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                                                                                                                                                                                22-DEC-2000;
02-MAR-2001;
                                                                                                                                                                                                                                                                    US2004072154-A1
                                                                                                                                                                                                                                                                                                                   cytostatic
                        Claim 1; SEQ ID NO
                                                          New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or
                                                                                                                     Morris
                                                                                                                                                                                                                    30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                                                            15-APR-2004
                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                             WPI; 2004-328562/30.
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                                                                                                                      DW.
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                                                                                                                                                                                                                                                                                                                                                                   carcinoma
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GTACAGCCAGGACTAC 91781
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2001US-00997722.
2001US-00034650.
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                                                                                                                    Engelhard
                                                                                                                                                                                2000US-00747377.
2001US-00798586.
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                 associated (CA) nucleic acid #43.
                      85; 29pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB
Pred. No. 1.3e
2; Mismatches
                        English
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1.3e+03;
0;
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The invention relates to new recombinant

nucleic acids. The invention

Neubauer A,

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cc expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for a bloactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nuclectide sequence, a cc carcinoma associated protein (CAP) a nectoded by a nuclectide sequence, a activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of carcinoma, a method of treating carcinoma, a method of treating carcinoma, a method of carcinoma or neutralising the effect of a CAP and a method of diagnosing carcinoma or cerivation of a gene comprise to a patient, removing a ccell sample from the patient and determining alterations in the carcinoma or activation of a gene comprise determining the expression or activation of a gene comprise determining the expression of the genes comprises the nucleic acid sequence in a first tissue type from the first individual and comparing the expression of the gene from a second normal tissue type from the first individual or a second a second normal tissue type from the first individual or a second carcinomas comprises binding an inhibitor to the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. The nucleic acid are useful for preparing a composition for diagnosing or treating carcinoma e.g., the nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specifically binds to the case of the case of the case of the comprises an antibody that specifically binds to the composition for diagnosing or treating cacids are useful for preparing a composition for diagnosing or treating cacids are useful for confident a useful of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 33
ADP74214/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 96600 BP; 27391 A; 19001 C; 20558
                                                                                                                                                                                                                                                                                                                                                                                                Equine herpesvirus 4 genome gM deletion mutant #2.
                                                                                                                                                                                                                                                                                                                                       virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
EHV-associated condition; Equine herpesvirus 4; EHV4; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004
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                                                                           19-JUL-2002; 2002DE-01033064
14-AUG-2002; 2002US-0403282P
11-APR-2003; 2003DE-01017008
                                                                                                                                                                                                    10-JUN-2004.
                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                  Equine herpesvirus 4
                                                                                                                                                            21-JUL-2003; 2003US-00624149
                                                                                                                                                                                                                                           US2004109873-A1
                                     (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GUACAGCCAGGACUAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTACAGCCAGGACTAC 91781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 12; L
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쁑
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29350 T; 0 U; 300 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 96600;
                                                                                                                                                                                                                                                                                                                                                  mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Claim 18; Page; 156pp; English.

New recombinant equine herpes and where protein gM has been or preventing EHV infections.

(EHV) virus free of heterologous elements, deleted, useful as a vaccine for treating

Herpes Virus (EHV) where

WPI;

2004-440311/41.

The invention describes a new recombinant Equine Herpes Virus (EHV) when the protein gM is absent, and the EHV is free of heterologous elements. Also described are: a nucleic acid coding for an EHV defined above; a vaccine preparation comprising the EHV or nucleic acid; obtaining a recombinant EHV; and a cell line for use in the method, where the gene encoding the protein gM is transfected into the cell line, and the cell line expresses gM. The vaccine comprising the EHV or nucleic acid encoding EHV is useful for treating and/or preventing EHV-associated condition, and for monitoring the therapeutic success. The recombinant EHV is useful as a vaccine against EHV infections. This sequence represents an Equine herpesvirus 4 genome in which nucleotides 92681-

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New recombinant equine herpes and where protein gM has been or preventing EHV infections.
The invention describes a new recombinant Equine Herpes Virus the protein gM is absent, and the EHV is free of heterologous
                                  Claim 19; Page; 156pp; English
                                                                                                                            Neubauer
                                                                                                                                                                        19-JUL-2002; 2002DE-01033064.
14-AUG-2002; 2002US-0403282P.
11-APR-2003; 2003DE-01017008.
                                                                                                                                                                                                                       21-JUL-2003;
                                                                                                                                                                                                                                                                   US2004109873-A1
                                                                                                                                                                                                                                                                                                   Equine herpesvirus
                                                                                                                                                                                                                                                                                                                         virucide; vaccine; Equine Herpes Virus; EHV; EHV-associated condition; Equine herpesvirus
                                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus 4 genome gM deletion mutant #3.
                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                           ADP74215;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP74215
                                                                                                                                                   (BOEH )
                                                                                                        2004-440311/41
                                                                                                                                                   BOEHRINGER INGELHEIM VETMEDICA GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 144486
                                                                                                                            Ziegler
                                                                                                                                                                                                                      2003US-00624149
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                            ü
                                                                 (EHV) virus free of heterologous elements, deleted, useful as a vaccine for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                      gM; vaccine;
4; EHV4; ds; mutant; mutein.
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(EHV) where

The invention describes a new recombinant Equine Herpes Virus (EHV) where the protein gM is absent, and the EHV is free of heterologous elements. Also described are: a nucleic acid coding for an EHV defined above; a vaccine preparation comprising the EHV or nucleic acid; obtaining a recombinant EHV; and a cell line for use in the method, where the gene encoding the protein gM is transfected into the cell line, and the cell line expresses gM. The vaccine comprising the EHV or nucleic acid encoding EHV is useful for treating and/or preventing EHV-associated condition, and for monitoring the therapeutic success. The recombinant EHV is useful as a vaccine against EHV infections. This sequence represents an Equine herpesvirus 4 genome in which nucleotides 92681-92731 and 93765-93865, comprising regions of the gM gene, have been deleted.

Claim 17; Page; 156pp; English

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RESULT 35
ADP74213/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Also described are: a nucleic acid coding for an EHV defined above; a vaccine preparation comprising the EHV or nucleic acid; obtaining a recombinant EHV; and a cell line for use in the method, where the gene encoding the protein gM is transfected into the cell line, and the cell line expresses gM. The vaccine comprising the EHV or nucleic acid encoding EHV is useful for treating and/or preventing EHV-associated condition, and for monitoring the therapeutic success. The recombinant EHV is useful as a vaccine against EHV infections. This sequence represents an Equine herpesvirus 4 genome in which nucleotides 92715-93824, comprising regions of the gM gene, have been deleted.
                                                                                                                                                                                                                           New recombinant equine herpes (EHV) virus free of heterologous and where protein gM has been deleted, useful as a vaccine for or preventing EHV infections.
                                                                                                                                                                                                                                                                                          WPI; 2004-440311/41.
                                                                                                                                                                                                                                                                                                                    Neubauer A,
                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2002; 2002DE-01033064
14-AUG-2002; 2002US-0403282P
11-APR-2003; 2003DE-01017008
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2003; 2003US-00624149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2004109873-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Equine herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equine herpesvirus 4 genome gM deletion mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP74213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP74213 standard; DNA; 145444 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 144486 BP; 35916 A; 36662 C; 36259 G;
                                                                                                                                                                                                                                                                                                                                                   (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76346 GGTACAGCCAGGACTA 76331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                    Ziegler C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               2002US-0403282P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
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Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35649 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 144486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                            elements,
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76346

GGTACAGCCAGGACTA 76331 GGUACAGCCAGGACUA 17 Conservative

Matches

14; N

Local

Similarity

80.0%; 87.5%;

Score 16; Pred. No.

1.4e+03; DB 12;

Length 144411;

2

Mismatches

0

Indels

0

Gaps

0

Sequence 144411 BP; 35893 A; 36645 C; 36246 G; 35627 T; 0 U; 0

93865, comprising regions of the gM gene, have been deleted.

RESULT 34

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RESULT 36
ADP742
XX
ADP742
XX
ADP742
XX
ADP742
XX
ADP742
XX
AC ADP742

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                         Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 145444 BP;
                                                                                                                                                                                                                                                                 The invention describes a new recombinant Equine Herpes Virus (EHV) where the protein gM is absent, and the EHV is free of heterologous elements. Also described are: a nucleic acid coding for an EHV defined above; a vaccine preparation comprising the EHV or nucleic acid; obtaining a recombinant EHV; and a cell line for use in the method, where the gene encoding the protein gM is transfected into the cell line, and the cell line expresses gM. The vaccine comprising the EHV or nucleic acid encoding EHV is useful for treating and/or preventing EHV-associated condition, and for monitoring the therapeutic success. The recombinant EHV is useful as a vaccine against EHV infections. This sequence represents the Equine herpesvirus 4 genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equine herpesvirus 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine; EHV-associated condition; Equine herpesvirus 4; EHV4; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus 4 genome seqid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-2002; 2002DE-01033064
14-AUG-2002; 2002US-0403282P
11-APR-2003; 2003DE-01017008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004109873-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant equine herpes (EHV) virus free of heterologous elements, and where protein gM has been deleted, useful as a vaccine for treating or preventing EHV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76346 GGTACAGCCAGGACTA 76331
76346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 80.0%;
Similarity 87.5%;
                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOEHRINGER INGELHEIM VETMEDICA GMBH.
                                                                                                                                         Similarity
GGTACAGCCAGGACTA 76331
                                                                                                                                                                                                                           145596
                                                 GGUACAGCCAGGACUA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ziegler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                               Conservative
                                                                                                                                                                                                                        BP; 36213 A; 36932 C; 36529 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36178 A; 36893 C; 36497 G; 35876 T; 0 U; 0
                                                                                                                                   80.0%;
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Pred. No.
                                                                                                               N
••
                                                                                                                                         Score 16; DB 12;
Pred. No. 1.4e+03;
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                                                                                                                                                                                                                              35922 T; 0 U; 0 Other;
                                                                                                                                                                   Length 145596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                     Indels
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RESULT 37

RESULT 38
ABD15945/c
ID ABD159
XX

ABD15945 standard; DNA; 411

ВP

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ADZ13116/c

ID ADZ13116;

XC ADZ13116;

XX ADZ13116;

XX Diagnosis; DNA microarray; microarray

Ex Murine cancer-associated genomic of the properties of the
                                                                                                                                                                                                                                                                                                                                                                                           cc associated (CA) nucleic acid, comprising two or more nucleic acid probes.

Ct isolated polypeptides encoded by a CA nucleic acid sequence, a compound ct that binds to a polypeptide, an isolated antibody or its fragment which co binds to a polypeptide, which is prepared by immunizing a host animal cc binds to a polypeptide, which is prepared by immunizing a host animal co mitted antibody and a compound ct the antigen or its antigen binding fragment, a composition comprising the polypeptide or its antigen binding cannot be expressing antibodies against the antibody and a carrier, a method of greening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a method of inhibiting expression of a CA nucleic acid in a cell. The CA nucleic acids are useful for detecting CA complete acids. The antibody is useful for detecting the presence of cancer cells in an individual which involves contacting cells from the individual with the antibody, where the detection of the complex correlates with the presence of cancer cells in an individual. The composition is useful for inhibiting growth of cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA cancer, for treating cancer and for inhibiting expression of a CA gene in a cancer, for treating cancer and for inhibiting expression of a CA cancer, for treating cancer and for inhibiting expression of a CA gene in cancer, for treating cancer and for inhibiting expression of a CA gene in cancer, for treating cancer and for inhibiting expression of a CA gene in cancer, for treating cancer and for inhibiting expression of a CA gene in cancer, for treating cancer and for inhibiting expression of a CA gene in cancer, for treating cancer and for inhibiting expression of a CA gene in cancer.
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                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine cancer-associated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 636; 198pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid array useful for detecting cancer associated nucleic acid, comprises two or more nucleic acid probés.
                                                                                                                                                                                          Local
42387
                                                                                                                                                       14;
                                                                                                                                                                                             Similarity
       GTACAGCCAGGACTAC
                                                              GUACAGCCAGGACUAC
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to a nucleic acid array for detecting a cancer
                                                                                                                                                                                                                                                                                                  59664 A; 56662 C; 57444 G; 61211 T; 0 U;
                                                                                                                                                                                          80.0%;
           42372
                                                                                                                                                           2
                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                Score 16; DB 14; Length 241748;
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                                                                                                                                                              Mismatches
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                                                                                                                                                                                                     1.4e+03
                                                                                                                                                           Indels
                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                      6767 Other;
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                                                                                                                                                          RESULT 39
                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                             bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial trugets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
      Bacterial infection; gene; ds; Pseudomonas aeruginosa infection,
                                     Pseudomonas aeruginosa polynucleotide #14815.
                                                                     29-JUL-2004
                                                                                                                             ABD16211 standard; DNA; 537 BP
                                                                                                                                                                                                                                                                                                                        Sequence 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 14549; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Pseudomonas aeruginosa polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polymucleotides encoding them. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a pathological infertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa polynucleotide #14549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABD15945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOME
                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                      346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-615309/58.
                                                                                                                                                                                                                                                               l Similarity
                                                                                                                                                                                                    AGCTACAGCCTGGACTACG 328
                                                                                                                                                                                                                                AGGUACAGCCAGGACUACG 19
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0074788P
98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9908-00252991
                                                                                                                                                                                                                                                                                                                     56 A; 128 C; 170 G; 57 T; 0 U; 0 Other;
                                                                    entry)
                                                                                                                                                                                                                                                                          79.0%;
78.9%;
                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deloughery
                                                                                                                                                                                                                                                                           Score 15.8;
Pred. No. 1
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                           1.2e+03
                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bush
                                                                                                                                                                                                                                                                                        Length 411;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Pseudomonas species using biochip technology. Sequences ABD01397-ABD017967 represent P. aeruginosa polynucleotides of the invention Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence data for the patent did not form the printed specification but was obtained in electronic format from USPTO at sequence data format part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                   ABV15922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial infection, for evaluating a compound, Buch as a puryperture, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs,
Homo sapiens
                                                        Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                Human prostate expression marker cDNA 15913
                                                                                                                                                                                                              13-SEP-2002
                                                                                                                                                                                                                                                                                                                               ABV15922 standard; cDNA; 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 537 BP; 76 A; 226 C; 160 G; 75 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 14815; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to Pseudomonas aeruginosa polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ABO82640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-615309/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US6551795-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 axis and treatment of pathological conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGUACAGCCAGGACUACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTACAGCCTGGACTACG 180
                                                                                                                                                                                                           (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nolling J, Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                               ₽₽
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
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20-FEB-2001; 2001WO-US005171.

23-AUG-2001

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ABV45722/c
ID ABV457
XX
AC ABV457
XX
XX Human
XX
Human
XX
Human
XX
Homo 8
XX
Homo 9
23-AUG
XX
20-FEE
PR 11-FEE
PR 11-FEE
PR 13-BUJUL
PR 13-DEC
XX
PR 09-JUL
PR 13-DEC
XX
PR 13-DEC
XX
PR 13-DEC
XX
MILL-
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is affilicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastasized in a patient; (f) assessing the aggressiveness or indolence of prostate cancer in a patient; (ii) is also useful as a pharmacodyanamic or pharmacogenomic marker; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel
                              16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 542 BP; 130 A; 111 C; 124 G; 173 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                pharmacogenomic
                                                                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 45713.
                                                                                                                                                                                                                                                                                                                                             16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                         ABV45722
                                                                                                                                                                       23-AUG-2001
                                                                                                            17-FEB-2000;
                                                                                                                                          20-FEB-2001;
                                                                                                                                                                                                      WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AGGUACAGCCAGGACUACG 19
|||:|||||||:||
90 AGGTAGAGCCAGGACTATG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                              prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
cogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA; 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0183319P.
; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-0255281P.
                              ; 2000US-0183319P.
; 2000US-0189862P.
2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
; 2000US-0255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                             (first entry
                                                                                                                                            2001WO-US005171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 5;
1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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(MILL-) MILLENNIUM

PREDICTIVE

MEDICINE INC

Claim 1; SEQ

ID NO

25544; 103pp; English

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RESULT 42
AAS89740/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 9040; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic d
                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #25544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS89740 standard; cDNA; 693
                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                       11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                          diagnostics, for responsible for biodiversity.
                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                             WPI; 2001-639362/73.
P-PSDB; ABG25553.
                                                                                                                                                          Drmanac
                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AGGUACAGCCAGGACUACG 19
                                                                                                                                                         RT,
                                                                                                                                                                                     HYSBQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTAGAGCCAGGACTATG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.0%;
nilarity 78.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 141 A; 124 C; 142 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                         Liu C,
                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monahan
                                                                                                                                                             Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      닖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8; DB 5;
. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 592;
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                                                                                                                                                                                                                                                                                                                                                                                 disorder;
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RESULT 43
ABL04139/c
ID ABL04139 standard; cDNA; 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences, (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC supplement protein expression or biological activity. The
CC involving aberrant protein expression or biological activity. The
CC involving aberrant protein expression or biological activity. The
CC diagnostics forensics, gene mapping, identification of mutations
CC conditions for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
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New isolated nucleic agenes from Drosophila interactions.
                                                                                                               WPI; 2001-656860/75.
P-PSDB; ABB60036.
                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                              23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 6899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL04139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 693 BP; 141 A; 192 C; 218 G; 142 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCACAGCCAGGACTAAGA 168
                                                                                                                                                                                            Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                           2000US-0191637P.
2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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84.2%;
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a and
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                                                                                                                                                                                              DWD,
                    detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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Pred. No. 1.
                                                                                                                                                                                              Myers EW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling

invention

18

Sequence

1023

BP; 142

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392 pct.

ü

329

G; 160

'n,

0

U; 0 Other;

ftp.wipo.int/pub/published_

Claim 1; SEQ ID NO 6899;

21pp + Sequence Listing; English.

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RESULT 44
ADS14617
ID ADS14
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                                        The present invention relates to a method for identifying a modulator of quorum sensing signalling in bacteria. The method comprises: providing a cell that comprises a quorum sensing controlled gene (ADS14446-ADS14798), where the cell is responsive to a quorum sensing signal molecule such that a detectable signal is generated; contacting the cell with a quorum sensing signal molecule in the presence and absence of a test compound; and detecting a change in the detectable signal. The method and modulator identified by the method are useful for treating a biofilm-associated disease or disorder, e.g. cystic fibrosis, ADIS, middle ear infections, acne, periodontal disease, catheter-associated infections, and medical device-associated infections. Note: The sequence data for this patent was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; Anti-HIV; Antimicrobial; quorum sensing signalling; bacterium; biofilm-associated disease; cystic fil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG1818-6-ABL30511) expressed DNA sequences (ABLG1818-6-ABL30511).
                                                                                                                                                                                                                                                                                                       Identifying a modulator of quorum sensing signaling in bacteria, for treating a biofilm-associated disorder, comprises contacting with a quorum sensing signal molecule in the presence and absence.
                                                                                                                                                                                                                                                                                                                                                                                                      Greenberg EP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB72072). The sequence data for this patent did not form part printed specification, but was obtained in electronic format difrom WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                          with a quorum sensing test compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2003; 2003US-00389647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAR-2004; 2004WO-US007467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004083385-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acne; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGUACAGCCAGGACUACG
                                                                                                                                                                                                                                                        SEQ ID NO 172; 233pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aeruginosa quorum sensing controlled
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                                                                                                                                                                                                                                                                                                                                                                                                        Schuster M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 A; 253
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antimicrobial; Immunosuppressive;
ling; bacterium; quorum sensing controlled
sease; cystic fibrosis; AIDS; middle ear ir
                                                                                                                                                                                                                                                                                                                                                                                                                                          FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
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Pred. No. 1.2e
2; Mismatches
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                                                                                                                                                                                                                                                                                                       presence and absence of
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infection;
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Length 1023;

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ABD16472
ID ABD
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                                                                                                                                        The invention relates to Pseudomonas aeruginosa polypeptides and the CC polynucleotides encoding them. The sequences are useful in diagnosis and the therapy of pathological conditions, as molecular targets for diagnostics, compoundly laxis and treatment of pathological conditions resulting from a CC bacterial infection, for evaluating a compound, such as a polypeptide, CC offective antibacterial targets, as targets for antibacterial drugs, cC including anti-P. aeruginosa drugs, as templates for recombinant CC components for diagnosis and/or treatment of P. aeruginosa-caused CC components for diagnosis and/or treatment of P. aeruginosa-caused CC infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed CC specification but was obtained in electronic format from USPTO at CC sequences auspho.gov/sequence.html
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Best Local Similarity
Matches 15; Conserv
                                                                        Query Match
Best Local
                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa polynucleotide #15076.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 15076; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOME
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || :||||| ||||:|||
166 AGCTACAGCCTGGACTACG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-615309/58.
   184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO82901.
                                                                         Similarity
 AGCTACAGCCTGGACTACG
                                AGGUACAGCCAGGACUACG
                                                                                                                    1044 BP;
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0074788P.
98US-0094190P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nolling J,
                                                                                                                    142 A; 404 C; 336 G; 162 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.0%;
78.9%;
                                                                        79.0%;
78.9%;
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Pred. No. 1
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                                                           2;
                                                           Score 15.8; D
Pred. No. 1.2e
2; Mismatches
   202
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. 1.2e+03;
2;
                                                                            1.2e+03
                                                                                         DB 11;
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                                                                Indels
                                                                                         Length 1044;
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Χü

RESULT 47

AAC99556

AAC99556 standard; cDNA; 1057 BP

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ARSSULT 46
ARSSULT 46
ARZ6123
ADZ61623
ADZ6163
AD
                                                                                                                                                                                                                                                                                                                        cc dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, cc and mouse embryonic skin, keratinocytes and neonatal foreskin fibroblasts, cells. Polypeptides of the invention may be used to treat inflammation, cc cells. Polypeptides of the invention may be used to treat inflammation, cc cancer and neurological diseases. The proteins may be used to stimulate ct the growth and motility of keratinocytes, to inhibit the growth of cancer cc cells, to modulate angiogenesis and tumour vascularisation, to modulate cc skin inflammation, to modulate epithelial cell growth and to inhibit combination of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle cc growth and developmental defects, skin wounds and hair follicle cc from several mouse, rat or human skin cell types. Sequences AAZ61606-Z61832 represent cDNA sequences AAZ61606-Z61832 represent cDNA sequences AAZ61606-CC with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences AAZ61607-Z61868, AAZ61766-Z61780, AAZ61812-Z61817 and AAZ61827-Z61829 encode proteins with one or more putative transmembrane cc domains
                                                                                                                       Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ61623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strachan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1998;
09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9955865-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 69-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides useful for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-072177/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                 Sequence 1057 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      including wounds and cancer
   1022
                                                                N
                                                                                                                             16;
                                                                                                                                                       Similarity
GCTACAGCCAGGACAACGA 1040
                                                                GGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sleeman M,
                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rat skin cell secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00069726.
98US-00188930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-NZ000051.
                                                                                                                                                                                                                                                     223 A; 315 C; 295 G;
                                                                                                                                                       79.0%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                             1;
                                                                                                                                                              Score 15.8; DB 3; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Onrust R,
                                                                                                                                                                                                                                                           224 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of various conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumble A,
                                                                                                                                                                                              Length 1057;
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                                                                                                                                          Indels
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                                                                                                                                                                   ABL34708
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Matches
                                                                                                                                                                                                                                                                                       Query Match
Rattus sp
                                            Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vuln
                                                                               Rat cDNA isolated from skin cells SEQ ID NO:
                                                                                                        04-APR-2002
                                                                                                                                ABL34708;
                                                                                                                                                      ABL34708 standard; cDNA; 1057
                                                                                                                                                                                                                                                                                                                                          tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammmatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                     The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 81; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-007495/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson JD,
Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB55898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2000; 2000WO-NZ000075
                                    immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200069884-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skin cell cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC99556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESIS RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; neurological disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001
                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                 1022
                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                              1057
                                                                                                                                                                                                                GCTACAGCCAGGACAACGA 1040
                                                                                                                                                                                                                                      GGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strachan L,
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00312283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:
                                  anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                  for examining expression patterns
                                                                                                                                                                                                                                                                                                            223 A; 315
                                                                                                                                                                                                                                                                         79.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                         Score 15.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                            C; 295 G;
                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sleeman
                                 cytostatic;
                                                                                                                                                                                                                                                                                                            224 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         .2e+03
                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z,
                                  neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kumble
                                                                                                                                                                                                                                                                                   Length 1057;
                                                                                                                                                                                                                                                              Indels
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                                            FXRRX
                                                                                                       8 × 2 ×
         Rubenfield MJ,
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RESULT 49
ABD16075/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABD16075 standard; DNA; 1452
                                         18-FEB-1998;
27-JUL-1998;
                                                                                                                                                                                      US6551795-B1
                                                                                                                                                                                                                                                                      antibacterial.
                                                                                                                                                                                                                                                                                          Bacterial infection;
                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa polynucleotide #14679.
                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                          ABD16075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1057 BP; 223 A; 315 C; 295 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watson JD,
Kumble KD;
                                                                                                     18-FEB-1999;
                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 83; 466pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-122020/16
(GENO-) GENOMB
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25-JUL-2000; 2000US-0221232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2001; 2001WO-NZ000099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1022 GCTACAGCCAGGACAACGA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
THERAPEUTICS CORP.
                                         98US-0074788P
98US-0094190P
                                                                                                     99US-00252991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%;
84.2%;
                                                                                                                                                                                                                                                                                          gene;
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                                                                                                                                                                                                                                                                                            ds;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 T;
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U;
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Nolling J,

Deloughery C,

Bush

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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABB17967 represent P. aeruginosa polymucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-615309/58.
P-PSDB; ABO82504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 14679; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1452 BP; 220 A; 453 C; 559 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        Rat; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
                 New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases.
                                                                                                                                                                                                                                                                                                                                          Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skin cell cDNA, SEQ ID NO: 447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC99799 standard; cDNA; 1890 BP
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                                                                                                                                                                                                        14-MAY-1999;
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                                                                                                                                                                                                                                                                                                            WO200069884-A2
                                                                                      WPI; 2001-007495/01
                                                                                                                                                                       (GENE-) GENESIS RES & DEV CORP LTD.
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15; Conserv
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|| :||||| |||:|||
AGCTACAGCCTGGACTACG 675
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                                                                                                                                       Strachan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                          99US-00312283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%;
78.9%;
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                                                                                                                                         Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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Pred. No. 1.3e+03;
                                                                                                                                          Sleeman
                                                                                                                                          Z,
                                                                                                                                          Kumble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                           Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                         Sequence 1890 BP; 388 A; 611 C; 463 G; 428 T; 0 U; 0 Other;
                                                                                                                                                                                                   oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 338-339; 352pp; English.
                                                                                                Local Similarity
  881 GCTACAGCCAGGACAACGA
                                                                               16;
                                       N
                                          GGUACAGCCAGGACUACGA 20
                                                                               Conservative
                                                                                                                                                                                                     for examining expression patterns
                                                                                                  79.0%;
84.2%;
                                                                                 1;
    899
                                                                                                       Score 15.8; DB 4;
Pred. No. 1.3e+03;
                                                                                      Mismatches
                                                                                                                            DB 4;
                                                                                                                            Length 1890;
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                                                                                          Gaps
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                                                                                                                                                                                                                                           Gallus gallus
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                         Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                          PO Box 88, Manchester,
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                                                                                                  Simon. Hubbard@umist.ac.uk.
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Pax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170, MSMg01. For BAC (Ibrary availability, please contact Kuniya Abe (abe@rtc.riken.jp). The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ezawa, K., Sa
Shiroishi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M.,
Bzawa, K., Saitou, N., Hattori, M., Sakaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG509048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence-SNP analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG509048.1 GI:48216461
                                                                                                                                                                                                                       Sequencing : TJ
                                                                                                                                                                            Vector
                                                                                                                                                                                                        LIBRARY
                                                                                                                                                                                                                                                     PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Following this first strand reaction, double-stranded CDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-923 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: brain; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
                                                                                                Location/Qualifiers
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
                                                                                                                                                     : pBACe3.6
: EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molossinus DNA,
                                                                                                                                 BCORI.
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747
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Moriwaki, K.
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AA855258
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                                                                                                 ORIGIN
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ORGANISM
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Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 331)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector to vector length is 332
Seg primer: -28ml3 rev1 BT from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
The WashU-HHMI Mouse BST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Euarchontoglires; Glires;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA855258.1 GI:2942796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vw70all.rl Stratagene mouse heart (#937316) Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:662836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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314 286 1810
           Conservative
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                                                                                                                                 /lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site 1:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
BcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
Adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1260284"
/sex="pooled"
                                                                                                                                                                                                                                                                                            dev_stage="13 day embryos"
                                                                                                                                                                                                                                                                                                                tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="mRNA"
strain="NIH Swiss"
                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sex="male"
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                           87.0%;
89.5%;
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      Score 17.4; DI
Pred. No. 1.1e-
1; Mismatches
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Pred. No.
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                             DB 1;
.1e+03;
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AI463924
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268
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
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Location/Qualifiers
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Putative full length read
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This read has been verified (found to hit its original self in the
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                                                                                                                                                                                                                                                            Conservative
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Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts:
Average insert size: 1.0 kb; Uni-ZAP XX Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Stratagene mouse heart (#937316)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
BooRI; Site_2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin_resistant)"
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286
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Pred. No. 1.1e+03;
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(E251666

CE251666 1 GI:35948584

GRS.

Canis familiaris (dog)

Canis familiaris (dog)

Canis familiaris

Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                    MB61p10C9 Mission Bay (San Diego, CA) uncultured marine virus genomic clone
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                                                                   Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego,
Tel: 6199941336
                                                                                                                                                                       Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F. Genomic analysis of uncultured marine viral communities Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                                                                    SSD
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                                                                                                                                      Contact: Rohwer F
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                                                   61959567
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                shotgun
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                               forest@sunstroke.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
Location/Qualifiers
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Eukaryotic Genomics,
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2; Mismatches 1;
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uncultured virus community
MB61p10C9, genomic survey
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2002)
Other_GSSs: OG2BX53TV
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                     Smail: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive,
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                                                                                                                                                                                                                                                                         methylation filtered.
Location/Qualifiers
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/db_xref="taxon:186617"
/clone="MB61p10C9"
                                                                                            /db_xref="taxon:4577"
/clone="zyMBMA0759I10"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector:_DBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="uncultured marine virus"
                                                                                                                                                                                                             organism="Zea mays"
|mol_type="genomic DNA"
                                                                                                                                                                                               /strain="873"
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Pred. No. 1.2e
2; Mismatches
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Pred. No. 1.2e+03;
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Similarity

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Quetier, F.,

nigroviridis part

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OG2BX53TV ZM_0.7_1.5_KB
Commic survey sequence
                                                                       AL238213.1 GI:7897348
GSS; genome survey sequence.
GSS; genome nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                               Tetraodon nigroviridis genome survey sequence T7 015I22 of library G from Tetraodon nigroviridis,
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Tel: 301-838-5843
Fax: 301-838-0208
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Other_GSSs: OG2BX53TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
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CG307140.1 GI:34224300
Bernot, A., Fizames, C. Saurin, W. and Weisser
                                   Roest Crollius, H., Jaillon, O.,
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Location/Qualifiers
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/clone=1b="ZM 0.7 1.5 KB"
/note="Vector: pBCSK:, Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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strain="873"
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., Wincker,P., Brottier,P., Quetier,F.,
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Pred. No. 1.2e+03;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM262 row: k column: 23
High quality sequence stop: 602.
                                                                                                                                                                                                          Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                 Unpublished (1999
                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
1 (bases 1 to 1016)
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Nat. Genet. 25 (2), 235-238 (2000)
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                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory
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/note="Genoscope sequence
end : T7"
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|mol_type="genomic DNA"
|db_xref="taxon:99883"
organism="Homo sapiens"
                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jaillon, O., Dasilva, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521
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Pred. No. 1.2e+03
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Length

<u>,</u>

Gaps

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Best Local Similarity Matches 17; Conserv
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AI757758
AI757758.1 GI:5151481
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: David Sibley, Ph.D.
WashU Merck Eimeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-Merck Eimeria tenella project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu)
Contact David Sibley (toxoest@borcim.wustl.edu)
information relating to organism, libraries, or
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eimeria tenella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 427)
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                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="IMAGE:1608974"
/tlssue_type="endometrium, adenocarcinoma cell line"
/tlssue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone=lib="NIH MGC 44"
/clone=lib="NIH MGC 44"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2: foots; cDNA made by oligo-dT priming. Directionally cloned into EccRI/KhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
/dev stage="Sporozoite"
//lab host="SOLR E. coli"
//lab host="SOLR E. coli"
//clone lib="Eimeria S5-2 Sporozoite stage"
//clone lib="Eimeria S5-2 Sporozoite stage"
//clone lib="Solr Eimeria S5-2 Sporozoite stage"
//note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: Bluescript Sk-; Site_1: EcoRI at reference from in vitro sporolated
and excysted occysts of E. tenella grown in chickens.

cDNA was synthesized from poly mRNA using an oligo-dT
primer containing a Xhol site. Following second strand
synthesis, EcoRI adapters were ligated to the cDNA and
products were size-selected on Sephacryl S500. cDNAs were
digested with EcoRI/Xhol and cloned into lambda Zap II
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01
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                                                                                                                                                                                                                                                                                             strain="LS18"
                                                                                                                                                                                                                                                                                                                                         organism="Eimeria tenella"
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89.5%;
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Pred. No. 1.2e+03;
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CE109731
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Best Local
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RESULT 11 AI757758/c

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Euteleostomi;

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tigr-gss-dog-17000324505919 fi
genomic survey sequence.
CE109731
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Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AGGUACAGCCAGGACUA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA Tel: 301-838-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                BG336492 109
602405476F1 NIH_MGC_21 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kirkness EF
                                                                             BG336492.1
                                                                                              mRNA sequence.
BG336492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 88.:
15; Conservative
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                        AGGUACAGCCAGGACUA 17
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Stratagene). Clones were converted to phagemids by mass excision using Exassist helper phage and SOLR cells (Stratagene). Insert sizes range from 1.2-2.9 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone_lib="Dog Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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88.2%;
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Pred. No. 1
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Dog Library Canis familiaris
                                                                                                                                    sapiens
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1.7e+03;
0;
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s cDNA
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                                                                                                                                      linear EST 27-FEB-2001 clone IMAGE:4543146 5',
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AQ515870
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Best Local Similarity
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320 bp DNA linear GSS 05-MAY-1999
HS_5235_A2_C05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=811 Col=10 Row=E, genomic_survey sequence.
                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases 1 to 320)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS
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ĀQ515870.1 GI:4748128
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Tissue Procurement: ATCC
                                                                                              High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLCM1224 row: g column:
High quality sequence stop: 460.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                           401 Queen Anne Avenue North, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA. Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.R. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UACAGCCAGGACUACGA 20
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(206) 616-3618
(206) 616-3887
1: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                    Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC_21"
/clone lib="NHH MGC_21"
/note="Torgan: placentry Vector: pOTB7; Site 1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="IMAGE:4543146"
tissue_type="choriocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%;
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Pred. No. 2e+03;
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                                                                              WA 98109, USA
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RESULT 15
AQ377301
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128
                                                                                                                                                                                                                                                                                                                                                                                                             Map Building Unpublished (1997) Other_GSSs: RPCI-11-162H24.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ377301 427 bp DNA RPCI-11-162H24.TV RPCI-11 Homo sapiens (RPCI-11-162H24, genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 811 row: E column: 10
                                                                                       Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 320
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                   Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 427)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                Class: BAC ends.
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                                                                       primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially disested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DN/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.8; DB 9; Pred. No. 2.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Jong, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
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REFERENCE
AUTHORS
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AJ691440
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KEYWORDS
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        DEFINITION
                                                                 RESULT 17
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                                                                                                                                                                                                                               Local
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AJ691440 KN261 Bos taurus c
AJ691440 1 GI:49424048
EST
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                                                                                                                                                                    μ
                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with the -minscore 20
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: SmaI 5' Seq Primer T3 Normalised library constructed from
bovine ovary. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGUACAGCCAGGACUACGA 20
BY471475 S27 bp mRNA linear BST 02-JAN-20 BY471475 RIKEN full-length enriched, melanocyte Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 432)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and BST resources for studying reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            embryo development in pigs and cattle 
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (cow)
                                                                                                                                                                                                                               Similarity
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                                                                                                                              AGGTATAGCCAGGACTATGA 360
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/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GDB:7562015"
/db_xref="taxon:9606"
/clone="RPCI-11-162H24"
                                                                                                                                                                                                                                                                                                           /note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site_2:
SmaI; Single pass sequencing. Normalised library
constructed from bovine ovary."
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                                                                                                                                                                                                                                                                                                                                                                       /clone="KN261-024_H05"
/tissue_type="ovary"
/clone_lib="KN261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                  xref="taxon:9913"
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                                                                                                                                                                                                                           84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     type="mRNA"
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e_lib="RPCI-11"
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                                                                                                                                                                                                          <u>ب</u>
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Pred. No. 2.2e+03;
                                                                                                                                                                                                                             Score 16.8; DB 1; Length 432; Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 bp
                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                         EST 02-JAN-2003
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COMMENT

1-7-22 Suehiro-cho, Tel: 81-45-503-9222

Yokohama, Kanagawa 230-0045, Japan

Fax: 81-45-503-9216

Email: genome res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Ishil,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission;
Computational Analysis of Full-Length Mouse cDNAs Compared with
Hayashizaki,Y. Direct Submission;
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease

Computer-based methods for the mouse full-length cDNA

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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BY471475
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
                                                                                                                                                                                                    12466851
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Simpson, A.J.
                                                                                                                                                                       High quality sequence start: 3 High quality sequence stop: 618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10737800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G270099G11"
                                                                                           organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                     ocation/Qualifiers
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'clone_lib="RIKEN full-length enriched, melanocyte"
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/mol_type="mRNA"
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                                                                           _xref="taxon:9606"
                                                       _stage="Adult"
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85.0%;
                                     lib="HN0036"
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Pred. No. 2.2e+03;
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Vector: puc18; ry was made by o
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cloning produc
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Best Local
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0201 row: G column: 17
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Utah (University of Utah Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reilly,M., Rose,M., Rose,R., Stokes,R., Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 54%)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B.
Dunn,D., Aoyagi,A., Barber,M., Meenen,B., Peder
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Peder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2M0201G17R Mouse 10kb plasmid Uclone UUGC2M0201G17 R, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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llarity 80.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid ends
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                             musculus C57BL/6J
                                                                                                                                                                                                                                     aboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0201G17"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from
                                                                                                                                                                                                                                                                             note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                   lab_host="B. coli strain XL10-Gold, T
clone_lib="Mouse_10kb_plasmid_UUGC2M
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Pred. No. 2.3e+03;
2; Mismatches 2
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                                                                                                                                                                                                                                                          (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           บับGC2M library Mus musculus genomic
ว ธนางey sequence.
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Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN285704 662 bp
17000532187304 GRN_ES Homo sapiens
CN285704 GI:47302118
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760
B1456742 690 bp mRNA linear EST 21-AUG-2001
603174629F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5253991 5',
mRNA sequence.
B1456742
                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                               Geron Corporation
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1 (bases 1 to 662)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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17; Conservative
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brandenberger R
                                                                                                                                                                                                                                                                      /note="oligo dr primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                 tissue_type="embryonic stem cells, cell lines
                                                                                                                                                                                                                                                                                                                          clone lib="GRN ES"
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85.0%;
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Pred. No. 2.3e+03;
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                                                                                                                                                                                          Score 16.8; DB 7;
Pred. No. 2.3e+03;
2; Mismatches 2;
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CC619972
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.R.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11641 row: j column: 08
High quality sequence stop: 627.
Location/Qualifiers
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1 (bases 1 to 690)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 728)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGMOE70TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC619972 728 bp DNA linear GSS 1970
OGWDE70TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0543L19,
                                                                                                                                                                                                                                                                                                                                                                          Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
CC619972
                                                                       Contact: Cathy Whitelaw
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Medical Center Drive, 301-838-5843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NCI_CGAP_Mam5"
/note="Organ: mammary Vector: pCMV-SPORT6; Site 1: Sall
/note="Organ: mammary Vector: pCMV-SPORT6; Site 1: Sall
Site 2: NotI; Cloned unidirectionally. Primer: Ōligo do
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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mol_type="mRNA"

strain="mix FVB/N, C578

db_xref="taxon:10090"
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Pred. No. 2.3e+03;
2; Mismatches 2
                              Rockville, MD 20850, USA
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                                                                                                      R.Site
R.Site
                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurmi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
                                                                                                                                                                Sequencing : TJ
LIBRARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 762)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG463520 762 bp DNA linear GSS 22 DEC-2004 Mus musculus molossinus DNA, clone: MSMg01-352G01.TJ, genomic survey
                                                                                                                                                                                                           PRIMERS
                                                                                                                                                                                                                        e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                Koyadai, Tsukuba, 305-
phone: 81-298-36-9189,
                                                                                                                                                                                                                                                                                Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1
                                                                                                                                                                                                                                                                                                            library availability, please contact Kuniya Abe
Tsukuba Institude, Bio Resource Center,
                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the mouse BAC library MSMg01. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 14 (12), 2439-2447 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shiroishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG463520.1 GI:48160776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 301-838-0208
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
                                                                               Location/Qualifiers
/organism="Mus musculus molossinus"
|mol_type="genomic DNA"
|sub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Zea mays"
/mol_type="genomic n
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: EcoRI
                                                                . 762
                                                                                                      BCORI
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Pred. No. 2.3e+03;
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Moriwaki, K.
                                                                                                                                                                                                                                                                                                                           (abe@rtc.riken.jp)
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C. and
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1 (Dases 1 to 773)

1 (Dases 1 to 773)

1 (Dases 1 to 773)

2 (Dases 1 to 773)

3 (Dases 1 to 773)

5 (Dases 1 to 773)

6 (Dases 1 to 773)

7 (Dases 1 to 773)

7 (Dases 1 to 773)

7 (Dases 1 to 773)
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSIIEa05F15.f OSIIEa Oryza sativa (indica cultivar-group) clone OSIIEa05F15 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arizona Genomics Inst
University of Arizona
Biological Sciences W
                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: gga aac agc tat gac cat
Plate: 05 row: F column: 15
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                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rmail: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 520 626 3967
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 AGGUACAGCCAGGACUACGA 20
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                                      Conservative
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                                                                                                                       /tissue_type="Leaf"
/dev stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIBa"
/note="Vector: pBluescript II KS +; Site_1:
XhoI; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                       db_xref="taxon:39946"
clone="OSIIBa05F15"
                                                                                                                                                                                                                                                                            cultivar="IR36"
                                                                                                                                                                                                                                                                                               organism="Oryza sativa (indica cultivar-group)"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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/clone="MSMg01-352G01.TJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                      84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ب</u>
                                                      Score 16.8; DB 6
Pred. No. 2.3e+03
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Pred. No. 2.
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                                                                         DB 6;
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CG269100/c
                                                     JOURNAL COMMENT
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AUTHORS
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VERSION
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CG269110
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                                                                                        TITLE
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CG269100
CG269100.1 GI:34181241
GSS.
Zea mays
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(Dases 1 to 784)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics
                                                                              Zea mays

Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 865)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maire Genomics
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Other_GSSs: OGXAK40TV
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                                                                                                                                                                                                                                                                        genomic survey sequence.
CG269110
CG269110.1 GI:34181251
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: TR
Class: methyla
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                              CG269110 865
OGXAK40TV ZM_0.7_1.5_KB Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays
                                                     Unpublished (2002)
Other_GSSs: OGXAK40TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cathy Whitelaw
                                  Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Medical Center Drive, Rockville, MD 20850, USA
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Location/Qualifiers
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/clone="lib="ZM_0.7_1.5 KB"
/note="Vettor: pBCSK-; Site 1: HincII; 0."
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 2.3e+03;
1; Mismatches 2;
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ZMMBMa0586H07,
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Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Numberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Unpublished (2002)
Other GSSB: OGNHE33TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 936)
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CG252727
CG252727.1 GI:34154817
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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genomic survey se
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                         Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                          Seq primer: TF
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                                                                            Similarity
AGGUACAGCCAGGACUACGA 20
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                                                             Conservative
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/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK:; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/mol_type="genomic Dl
/strain="B73"
                                                                                                                                     /clone="ZMMBMa0577D21"
/clone=11b="ZM 0.7_1.5KB"
/note="Vector: pBCSK:, Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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85.0%;
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1.5 KB Zea mays genomic clone ZMMBMa0577D21,
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Pred. No. 2.4e+03
1; Mismatches
                                                             1;
                                                                            Score 16.8; DB 10
Pred. No. 2.4e+03;
                                                               Mismatches
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                                                                                            DB 10;
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RESULT 29
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BZ553930/c
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                                                                                                                                                                AUTHORS
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pacs1-60
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                                                                                                                                                                                                                                                                                                                                                                                 BF214228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Washington
Box 352145, Seattle, WA 98105-2145,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
J. Bacteriol. (2002) In press
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                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                         BF214228.1 GI:11107814
                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Chris K. Raymond
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                                cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                       Contact: Robert Strausberg, Ph.D.
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(bases 1 to 965)
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/clone_lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
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strain="1-60"
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Incyte Genomics, Inc.
: MGC clone distribution information can be
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Pred. No. 2.4e
1; Mismatches
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                                   Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole-Genome-Sequence variation Psedomonas aeruginosa library J. Bacteriol (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, B.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.
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Plate: LLCM937 row: b column:
                                                                                                                                                                                                                                                                                                         Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                     University of Washington
Box 352145, Seattle, WA
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                                                                                                                                                                                                                                                                              Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgccttggcc); Site 2: SfiI (ggccgccttggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and collows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_55"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"
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                                         'clone="pacs2-164_4207"
'clone_lib="pacs2-164"
'note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ' adaptor sequence:
'-ATTCTAGAGGCCGAGGCCGACATG-dT(30)BN-3' (where B = A,
                                                                                                                                           strain="2-164"
                                                                                                                                                                                organism="Pseudomonas
                                                                                                              db_xref="taxon:287"
                                                                                                                                                               mol_type="genomic DNA"
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85.0%;
                                                                                                                                                                                                              .1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 2;
Pred. No. 2.4e+03;
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                                                                                                                                                                                     aeruginosa"
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SOURCE
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CL023089
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DN675670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1210)
Kremisk, C., Carter, J., McPherson, J., Warren, W., Gr Mardis, B. and Wilson, R.

A physical map of the xenopus tropicalis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CH216-15N1_RM1.1 CH216 Xenopus tropicalis
genomic survey sequence.
CL023089
CL023089.1 GI:40464902
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                         DN675670 1217 bp mRNA line
CFW87-H01.yld-s SHGC-CFW Gasterosteus aculeatus
CFW87-H01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCACTATAGGGAGA
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CL023089
                                                              Gasterosteus aculeatus (three spined stickleback)
                                                                                               DN675670.1 GI:61995849
                                                                                                            DN675670
                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                             AGGUACAGCCAGGACUACGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 147 quality sequence stop: 495.
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Yector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="CH216-15N1"
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85.0%;
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Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                             Score 16.8; DB 10
Pred. No. 2.5e+03;
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                                                                                                                                                         EST 29-MAR-2005
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AUTHORS
                                                                                                                                                                                                    RESULT 33
AK050767/c
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Matches 16
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                                                                 Mus musculus
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AK050767

AK050767

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AK050767

AK050767

AK050767

ANA linear HTC 03-APR-:
Mus musculus 9 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:D030018D22 product:unclassifiable, full
insert semicore
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Plate: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 947
Tel: 650 320 5917
Fax: 650 320 5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
Contact: Grimwood, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1217)
Kingsley,D.M., Peichel,C., Balabahdra,S.,
Schmutz,J. and Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gasterosteidae; Gasterosteus.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                   AK050767
AK050767.1 GI:26094105
                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                           HTC; CAP trapper.
                                                                                                                                                                                                                                                             insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |:||||||||||:|| | AAGTACAGCCAGGACTACAA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGUACAGCCAGGACUACGA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTTCTAGATCGCGAGGGGCCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and ECORV sites of Express 1. Note that the ECORV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the ECORV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:

http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary_library_was transformed and amplified in_DHJOB_(T1 phage resistant) bacteria. Clones available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.openbiosystems.com/stickleback"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from Open Biosystems:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="mixed male and female"
/tissue_type="gills"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
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note="Vector: Express 1; Total and poly A+ RNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="CFW87-H01"
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Pred. No. 2.5e+03;
2; Mismatches 2; Indels 0
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                                                                                              Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                            HTC 03-APR-2004
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                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

E 6 (bases 1 to 303)

E 8 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanaggaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itch,M., Kagawa,I., Kasukawa,T., Katch,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakar,K., Sakasaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakasaki,Y., Saito,R., Shibata,K., Shinagawa,A., Shiraki,T., Sacati, M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Teurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome cDNA library was prepared Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Larmingl, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FANTOM Consortium and the RIKEN Genome Exploration Research
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409, 685-690 (2001)
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                                                                                                                                                                                                             organism="Mus musculus"
|mol_type="mRNA"
tissue type="whole body"
clone Tib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                           db_xref="FANTOM_DB:D030018D22"
                                                                                   one="D030018D22"
                                                                                                               xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/bac_end
Plate: 453 row: P column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lones are derived from the mouse contact Pieter de Jong Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Other_GSSs: RPCI-23-453P19.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23
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Jong,P. and Fraser,C.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ106943.1 GI:7759999
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            /clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Forgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
Recorl; Site_2: Ecorl; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                det
                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="RPCI-23-453P19"
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Pred. No. 2
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Query Match Best Local Matches 1

Similarity

82.0%; 83.3%;

Score 16.4; DB 9; Pred. No. 3e+03;

Length 176;

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Conservative

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Contact: Ralph Quatrano Leeds/Wash U Moss EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Libraries were constructed by Dr. Stavros Bashiardes as part of the
Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and
Washington Univ. in St. Louis (USA) DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
Seq primer: -40RP from Gibco.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;

Bryopeida; Funariidae; Funariales; Funariaceae; Physicomitrella.

1 (bases 1 to 225)
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Fax: 314 286 1810
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/lab host="DHIUB"
/clome lib="Moss EST library PPN"
/clome lib-moss EST library PPN"
/knoi; Construction of the cDNA library was carried out xhoi; Construction of the cDNA library was carried out using Stratagenes 'UniZAP - CDNA synthesis kit'. CDNA was constructed using an oligo dT primer/linker that contains a Xhoi site within it. Following ds cDNA synthesis,
ECORI adapters were ligated to the blunt ends and sample was digested with Xhoi. The result is cDNA with an ECORI sticky end on one side and a Xhoi sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using gold gigapackaging extracts. Library was grown in XLIBlue was excision using Stratagens 'Mass excision kit' that uses excision k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Physcomitrella patens"
/mol_type="mRNA"
/db_xref="taxon:3218"
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/tissue_type="protonemata: 7 day
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RESULT 36
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AUTHORS
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Matches 15; Conserv
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.
1 (bases 1 to 305)
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
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                                                                                                                                          16:
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AGGGACAGCCÁGGACTÁC 35
                                                                 AGGUACAGCCAGGACUAC 18
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                       /clone lib="CT0263"
/clone Trygan: colon; Vector: puc18; Site_1: SmaI; Site_2:
/note="Trygan: colon; Vector: puc18; Site_1: SmaI; Site_2:
/note="Trygan: colon; Vector: parent spouducts derived SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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83.3%;
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pred. No. 3.1e+03;
2; Mismatches 1
                                                                                                                                          1:
                                                                                                                                                                              Score 16.4; DB 1;
Pred. No. 3.2e+03;
                                                                                                                                                 Mismatches
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Bapiens cDNA,
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                                                                                                                                                                                                                   Length 305;
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REFERENCE
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BG408882
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ORGANISM
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VERSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a Clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)

Trace considered overall poor quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Location/Qualifiers
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Fax: 314 286 1810
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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BG408882.1 GI:13315227
EST.
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gb81c06.y1 Moss EST library PPG Physcomitrella patens cDNA clone
PEP SOURCE ID:PPG CopyA-100612 5' similar to TR:081361 081361 40S
RIBOSOMAL PROTEIN S8. ', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physcomitrella patens
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                      second strand, to amplify the double stranded DNA, and to incorporate dUTP containing sequences into the ends of the double stranded cDNA. This DNA was size selected and cloned into pampl using the CloneAMP pampl System (Life Technologies, GibcoBRL) for cloning amplification products by a non-restriction site dependant process. The cloning was directional based on sequence asymmetry introduced at the ends during PCR amplification. The 3' CDNA ends are proximal to the NotI site of the multiple cloning site in pample. This annealing mixture was transformed into chemically competent DH10B, cells and selected for amplicallin resistant growth. The resulting clones (about 330,000) were pooled to make the library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: panyl; construction of the cDNA library was performed by Dr. W. Gregg Clark using a modification of the cDNA synthesis protocol developed in the laboratory of Dr. Michael Lovett by Dr. Yulia Korshunova (personal communication). First polyA + RNA was isolated from total gametophore RNA using oligo dT magnetic beads. Following this, first strand cDNA synthesis was performed on the bead-bound polyA + RNA, during which an oligonucleotide anchor sequence was incorporated onto the 5'-ends of the CDNA. PCR amplification was then used to synthesize the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xréf="taxon:3218"
/clone="PBF_SOURCE ID:PPG_CopyA-100612"
/rissue_type="gametophore: 30 day old t:
ammonium-grown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Physcomitrella patens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  day old tissue,
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Query Match

Score 16.4;

DB 2;

Length 307

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ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                       RESULT 39
CZ689611
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AUTHORS
TITLE
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VERSION
KEYWORDS
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BP427629
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                                                                                              REFERENCE
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   JOURNAL
                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                 74 AGGTACAGCCAGGGCTAC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Miller, C., Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A. OMAP (Oryza Map Alignment Project) - Purdue University Unpublished (2004)
                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.
1 (bases 1 to 341)
                                                                                                                                                                      Oryza alta
Oryza alta
                                                                                                                                                                                                           GSS
                                                                                                                                                                                                                             genomic survey sequence. CZ689611 CZ689611.1 GI:70810763
                                                                                                                                                                                                                                                                                  CZ689611 341
OA_BBa0160F02.r OA_BBa Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AGGUACAGCCAGGACUAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Molecular Neurogenesis
RIKEN Brain Science Institute
2-1 Hirosawa, Wako, Saitama 351-0198, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 308)
Furuichi, T. and Sato, A.
Gene expression during the postnatal cerebellar development Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mol-neurogenesis@brain.riken.go.jp, URL:
http://www.brain.riken.go.jp/labs/lmn/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-48-467-5906
Fax: 81-48-467-6079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP427629 Mus musculus cerebellum E18-P56 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Teiichi Furuichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FD1374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="cerebellum"
/dev_stage="B18-P56"
/clone_lib="Mus musculus cerebellum B18-P56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="FD1374"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 3
Pred. No. 3.3e+03
2; Mismatches
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                                                                                                                                                                                                                                                                                    alta
                                                                                                                                                                                                                                                                              DNA linear GSS 14-JUL-2005 genomic clone OA_BBa0160F02 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
                                                                      Wissotski, M., Yost, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMMENT
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AW598793
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                                             FEATURES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bource
                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AĞGTAÇAĞÇAAĞĞAÇTAÇ 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clipping.
Plate: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s.
Bases 108-448 of the raw sequence (length 1010) were retained after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purdue University
915 W. State St., West Lafayette, IN 47907,
Tel: 7654963621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Scott A. Jackson
Jackson Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW598793 373 bp mRNA linear EST 22-ga88b10.y1 Moss EST library PPU Physcomitrella patens cDNA PRP SOURCE ID:PPU161320 5' similar to SW:RS8_ORYSA P49199 4 RIBOSOMAL PROTEIN S8. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGUACAGCCAGGACUAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: sjackson@purdue.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 7654967255
                                                            Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk) seq primer: -40RP from Gibco High quality sequence stop: 262.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 373)
Quatrano,R., Bashiardes,S., Cove,D., Cuming,A., Knight,C., Quatrano,R., Bashiardes,S., Cove,D., Cuming,A., Knight,C., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW598793.1 GI:7286306
                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                               Contact: Ralph Quatrano
Leeds/Wash U Moss BST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Physcomitrella patens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physcomitrella patens
                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:52545"
/clone="OA_BBa0160F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="young leaves"
/lab_host="pH1OB-T1 phage resistant"
/clone_lib="OA_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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organism="Physcomitrella patens"
                                           Location/Qualifiers
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 10;
Pred. No. 3.3e+03;
                                                                                                                                                                                                                                                                                                                       Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                                                                                       3
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REFERENCE
AUTHORS
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SOURCE
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ACCESSION
VERSION
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CV320420/c
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                   i (bases 1 to 385)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, B., Garcia Correa, R., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., Brunstein, A., Goliveira, P.S., Bucher, P., Jongeneel, C.V., and O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CV320420 385 bp mkNA 11Hear CW3-CN0094-230101-645-b02 CN0094 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CV320420.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV320420
                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                   Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                           sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97
                                                      Rua Prof. Antonio Prudente 109, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTACAGCCAGCACTACG 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unizar arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XLIBlue MRF, cells and amplified. The library was excised by mass excision using Stratagens 'Mass excision kit' that uses exassist as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. Solk cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."
+55-11-2704922
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/clone lib="Moss EST library PPU"
/clone lib="Moss EST library PPU"
/clone Tyector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Yector: pBluescript SK-; Site_1: CDNA
xho; Construction of the cDNA library was carried out
was constructed using an oligo dT primer/linker that
was constructed using an oligo dT primer/linker that
contains a XhoI site within it. Following ds cDNA
synthesis, EcoRI adapters were ligated to the blunt ends
synthesis, EcoRI adapters were ligated to the blunt ends
and sample was digested with XhoI. The result is cDNA
with an EcoRI sticky end on one side and a XhoI sticky
end on the other. This cDNA was ligated directionally in
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/db xref="taxon:3218"
/clone="pEp SOURCE ID:PPU161320"
/tissue_type="protonemata: 7 day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lab_host="DH10B"
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83.3%;
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Pred. No. 3.3e+03;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                                                   Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 bp mRNA linear E
BJ949932 pphf full-length cDNA libary Physcomitrella
patens cDNA clone pphf5o22 5', mRNA sequence.
BJ949932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ949932.1 GI:67577765
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. http://www.ludwig.org.br.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tshini@genes.nig.ac.jp
Protonemata were inoculated on BCDATG medium for every ca. 5 days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Physcomitrella patens EST at a stage of the first asymmetric cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTACAGCCAGGACTTC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 390)
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/clone lib="CN0094"
/note="Torgan: colon normal; Vector: puc18; Site 1: SmaI;
/note="Torgan: colon normal; Vector: puc18; Site 1: SmaI;
/note="Torgan: colon normal; Vector: puc18; Site 1: SmaI;
/note="Torgan: colon normal; Vector: Patent application of derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                               protoplasts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
clone lib="pphf full-length cDNA libary"
/note="Protonemata were inoculated on BCDATG medium for
every ca. 5 days. Protoplasts were isolated from the
                                                                                                            tissue_type="regenerated protoplasts (chloronemata)"
dev_stage="at the first asymmetric cell division of
                                                                                                                                                             /sub_species="patens"
/db_xref="taxon:145481"
/clone="pphf5022"
                                                                                                                                                                                                                                               organism="Physcomitrella
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 low stringency conditions."
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Pred. No. 3.4e+03;
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GGUACAGCCAGGACUACG Conservative

Matches Query Match

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82.0%;

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KEYWORDS
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BJ949577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 35 under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 395)
Fujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
Physcomitrella patens EST at a stage of the first asymmetri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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BJ949577
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Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ949577.1 GI:67576753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                  light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library."
                                                                                                                     /note="Protonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25C under continuous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructing a full-length cDNA library."
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light for 2-
                                                                                                                                                                                                                                                  tissue_type="regenerated protoplasts (chloronemata)"
/dev_stage="at the first asymmetric cell division of
                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/sub_species="patens"
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                                                                                                                                                                                                                                                                                                                                                                                                       organism="Physcomitrella patens subsp. patens"
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clone="pphf4c21"
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83.3%;
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Pred. No. 3.
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Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
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RESULT 44
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Quatrano,R., Bashlardes,S., Cove,D., Cuming,A., Knight,C.,
Quatrano,R., Bashlardes,S., Cove,D., Martin,J., Wylie,T.,
Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T.,
Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,B.,
Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
Leeds/Wash U Moss EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp mRNA linear EST 21-AUG-20 gc51e03.y1 Moss EST library PPN Physcomitrella patens cDNA clone PEP SOURCE ID:PPN180905 5' similar to SW.RS8 MAIZE Q08069 40S RIBOSOMAL PROTEIN S8. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Libraries were constructed by Dr. Stavros Bashiardes as part of the Physicomitrella ST program (PB) at the Univ. of Leeds (UK) and Washington Univ. In St. Louis (USA) DNA sequencing by Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk) Trace considered overall poor quality
High quality sequence stop: 1.
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Contact: Ralph Quatrano
Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physcomitrella patens Physcomitrella patens
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Fax: 314 286 1810
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Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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                                                                                                                                                                        /clone lib="MOSS EST library PPN"
//clone | Typector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Construction of the cDNA library was carried out
using Stratagenes 'UniZAP - cDNA synthesis kit'. cDNA was
constructed using an oligo dT primer/linker that contains
a XhoI site within it. Following ScDNA synthesis,
EcoRI adapters were ligated to the blunt ends and sample
was digested with XhoI. The result is cDNA with an EcoRI
sticky end on one side and a XhoI sticky end on the other.
This cDNA was ligated directionally in UniZAP arms. The
vector is designed containing the pBluescript sequence as
well as lambda DNA and cDNA is cloned within this
pBluescript sequence. The vector was then packaged using
Gold gigapackaging extracts. Library was grown in XLIBlue
MRP' cells and amplified. The library was excised by mass
excision using Stratagens 'Mass excision kit' that uses
exassist as a helper phage that releases the pBluescript
sequence and circularises it as single stranded plasmids
that are then packaged (by helper phage) and secreted out
of the host cell as phagemids. SOLR cells were transformed
with phagemids and the library was plated out on LB-amp
plates to select for transformants. Approximately
                                stranded plasmid library was recovered by using Quiagen Midi prep kit. 2 micro grams of each library were used transform DH10B cells by electroporation."
                                                                                                                                        places to select for transformants. Approximately 1,000,000 colonies were grown and recovered. The double
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|mol_type="mRNA"
|db_xref="taxon:3218"
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/tissue_type="protonemata: 7 day
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                                                                                                                                                                                                                                                                                           Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Wattahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Chazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                 Location/Qualifiers
/tissue_type="lung"
/cell_line="RCB-0558 LLC"
                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                       organism="Mus musculus"
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83.3%;
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Pred. No. 3.4e+03;
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  371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp
Protonemata were inoculated on BCDATG medium for every ca. 5 days.
Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PMYSCObase (http://moss.nibb.ac.jp).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ959669 pphf full-length cDNA patens cDNA clone pphf3j20 3', BJ959669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division of protoplasts 
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujita,T., Nishiyama,T., Shin-i,T., Kohara,Y. and Hasebe,M. Physcomitrella patens EST at a stage of the first asymmetric cell
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Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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                                                                                                     Similarity
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GGTACAGCCAGCACTACG 354
                                        GGUACAGCCAGGACUACG 19
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                                                                                Conservative
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                                                                                                                                                                                                                                                         /note=TProtonemata were inoculated on BCDATG medium for every ca. 5 days. Protoplasts were isolated from the protonemata, further incubated at 25C under continuous
                                                                                                                                                                                 constructing a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Physcomitrella patens subsp. patens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                 tissue_type="regenerated protoplasts (chloronemata)"
dev_stage="at the first asymmetric cell division of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                           ght for 2-3 days. The regenerated cells, which were cells at a stage during the first asymmetric cell vision, were collected. Total RNA was extracted for nstructing a full-length cDNA library."
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lone="pphf3j20"
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83.3%;
                                                                                                 82.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              species="patens"
                                                                                                                                                                                                                                                                                                                       lib="pphf full-length cDNA libary"
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Pred. No. 3.4e+03;
                                                                                                 Score 16.4;
Pred. No. 3.
                                                                              Mismatches
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                                                                                                     .4e+03;
                                                                                                                      DB 3;
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                                                                                                                  Length 404;
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                                                                                Indels
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RESULT 47

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RESULT 48
BJ960521/c
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LOCUS
DEFINITION
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SOURCE
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                          AUTHORS
                                                                                                                                   ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                      auye0521 pphf full-length cDNA libary Physcomitrella patens cDNA clone pphf4c21 3', mRNA sequence.
BJ960521
BJ960521.1 GI:67700288
EST.
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Physcomitrella patens subsp. patens
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

(bases 1 to 406)
Pujita, T., Nishiyama, T., Shin-i, T., Kohara, Y. and Hasebe, M.
Physcomitrella patens EST at a stage of the first asymmetric cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GGUACAGCCAGGACUACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zhonghuai Xiang
Southwest Agricultural University
Chongqing Beibei
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Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CK499977.1 GI:40860719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 86-23-68251123
Fax: 86-23-68251128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 306 (5703), 1937-1940 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xzh@swau.cq.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Bombyx mori"
'mol_type="mRNA"
'strain="DaZhao(P50)"
'db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dev_stage="5th-instar day-3 larva"
clone_lib="swb"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="midgut"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="mixed"
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83.3%;
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COMMENT
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                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp
Protonemata were inoculated on BCDATG medium for every ca. 5 days.
Protoplasts were isolated from the protonemata, further incubated at 25C under continuous light for 2-3 days. The regenerated cells, which were rich in cells at a stage during the first asymmetric cell division, were collected. Total RNA was extracted for constructing a full-length cDNA library. The database of the EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).
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                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 413)
Young, J.M., Friedman, C., Williams, E.M., Ross, J.A., Tonnes-Priddy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGUACAGCCAGGACUACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2005)
                                                                                                           Barbara Trask, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Boo
                                                                                                                                                                                                                         Different evolutionary processes shaped the mouse olfactory receptor gene families Hum. Mol. Genet. 11 (5), 535-546 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH405922 413 bp DNA linear Gi
RPCI-23-114A5.SP6B RPCI-23 Mus musculus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH405922
BH405922.1 GI:17460837
Email: jayoung@fhcrc.org
Young,J.M., Swartzell,S., Friedman,C.,
                                              Tel: 206 667 1471
Fax: 206 667 6524
                                                                                           98109-1024, USA.
                                                                                                                                                                               Contact: Young JM
                                                                                                                                                                                                                                                                                             and Trask, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCI-23-114A5,
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/db_xref="taxon:145481"
/clone="pphf4c21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Physcomitrella
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="regenerated protoplasts (chloronemata)"/clev_stage="at the first asymmetric cell division of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                Box 19024, Seattle,
  Tonnes-Priddy, L., Lane, R.P.,
                                                                                                                                                                                                                                                                                                                  Ross, J.A., Tonnes-Priddy, L.
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                                                                                                                                                                                                                                                                          and human
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AZ222766
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ORGANISM
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Matches
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mes 15; Conserv
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55 AAGTACAGCCAGGACTAC 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 bp DNA linear GSS 14-JUN-2000 RPCI-23-46J7, TJ RPCI-23 Mus musculus genomic clone RPCI-23-46J7, represent a company and a co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other_GSSs: RPCI-23-46J7.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 426)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Kr
Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomic survey sequence. AZ222766
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                                                                                                                                                                                                                                                                                                                   Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 46 row: J column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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                                                                                                                                                                                                                     Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site 1:
/note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site 1:
BCORI; Site 2: ECORI; Female C57BL/6U mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
BCORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
/organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                             Location/Qualifiers
1. .426
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Query Match 82.0
Best Local Similarity 83.3
Matches 15; Conservative
1 AGGUACAGCCAGGACUAC 18
                                                                                                                                                                                                                   /lab_host="DH10B"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Forgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Forgan: Kidney/Brain; Vector: pBACe3.6; Site_and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="C57BL/6J"
db_xref="taxon:10090"
clone="RPCI-23-46J7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ex="Female"
                                                                        82.0%; Score 16.4; DB 9; Length 426;
83.3%; Pred. No. 3.4e+03;
ative 2; Mismatches 1; Indels
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Search completed: March 18, 2006, 20:03:51 Job time: 1948.08 secs

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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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RESULT 1
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Sequence 3156, Application US/0
Patent No. 6902887
GENERAL INFORMATION:
APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7959
LENGTH: 735
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Best Local :
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                                                                                                                                    Application US/09533559
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85.0%;
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3 US-09-252-991A-12484
2 US-08-453-472-3
2 US-08-453-952-3
2 US-08-453-952-3
3 US-08-462-903-3
2 US-08-463-252-30
3 US-08-463-252-30
3 US-08-463-232-30
3 US-08-463-232-30
3 US-08-463-232-30
3 US-09-100-546-30
3 US-09-100-546-30
3 US-09-100-546-30
3 US-09-100-546-30
3 US-09-110-546-30
3 US-09-110-546-30
3 US-09-110-546-30
3 US-09-110-546-30
3 US-09-113-804-4
3 US-09-252-991A-2650
3 US-09-153-804-4
3 US-09-252-991A-12989
3 US-09-153-804-4
3 US-09-252-991A-13907
3 US-09-252-991A-13907
3 US-09-252-991A-13907
3 US-09-252-991A-13907
3 US-09-252-991A-13907
3 US-09-252-991A-13907
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Pred. No. 1.4e+02;
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PATENT NO. 6551795

GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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LENGTH: 246
TYPE: DNA
CRGANISM: Fusarium venenatum
US-09-533-559-3156
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US-09-270-767-12904
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US-09-252-991A-14549/c
TYPE: DNA
ORGANISM: Pseudomonas
US-09-252-991A-14549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12904
LENGTH: 1564
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TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REPERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 1999-03-22
RAPLIER FAPILICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                          Sequence 14549,
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                                                         LENGTH:
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87.5%;
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                              US-09-949-016-64679
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; ORGANISM: Drosophila melanogaster
US-09-270-767-11626
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US-09-270-767-11626/c
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US-09-252-991A-14815
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                                                  RESULT 7
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Sequence 64679, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
EQ ID NO 11626
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 62517
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 537
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                           ENGTH: 576
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Local Similarity 78.9%;
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                                                                                                                               1 AGGUACAGCCAGGACUACG 19
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78.9%;
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78.9%;
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Pred. No. 3.9e+02;
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Pred. No. 3.
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Pred. No. 3.9e+02;
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US-09-949-016-64681

equence 64681,

Application US/09949016

tent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

NUMBER: US/09/949,016

RESULT 9

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; ORGANISM: Human
US-09-949-016-64680
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US-09-949-016-64680
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TYPE: DNA
ORGANISM: Human
S-09-949-016-64679
                                                                                                                                                                                                                                             SEQ ID NO 64680
                                                                                Matches
                                                                                                                      Query Match
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Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR ETLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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                                                                                                 Local Similarity
  309
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                                                                              16;
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GGCACAGCCAGGACTAAGA 327
                                 GGUACAGCCAGGACUACGA 20
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                                                                              Conservative
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84.2%;
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                                                                                               79.0%;
84.2%;
                                                                                                 Score 15.8;
Pred. No. 3
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Pred. No. 3.
                                                                              Mismatches
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OF DETECTION AND USES THEREOF
                                                                                                                    Length 601;
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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: And Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 뭉
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US-09-252-991A-15076
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US-09-188-930-18
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ORGANISM: Human
-09-949-016-64681
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NUMBER OF SEG ID NOS: 33142
SEG ID NO 15076
LENGTH: 1044
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION 1998-07-27
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRI
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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78.9%;
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US-09-188-930-18
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US-09-312-283C-18
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 14679
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APPLICANT: Kumble, Krishanand D.

TITLE OF INVENTION: Compositions Isolated from Skin Cells

TITLE OF INVENTION: and Methods for Their Use

FILE REFERENCE: 11000.1011c2

CURRENT APPLICATION NUMBER: US/09/312,283C

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 425
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LOCATION: (45)...(45)
NAME/KEY: unsure
LOCATION: (53)...(53)
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. RUBENFION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                              Sequence 14679, App
Patent No. 6551795
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Best Local Similarity
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthe
APPLICANT: Onrust, Rene
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LOCATION: (116)...(116)
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LOCATION: (118)...(118)
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ORGANISM: Mouse
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Sleeman, Matthew
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84.2%;
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Pred. No. 4e
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4e+02;
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; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-230
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                           Query Match
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Best Local Similarity
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                                                                                                                                                                                           TITLE OF INVENTION: Compositions TITLE OF INVENTION: and Methods
                                                                                                                                                                 CURRENT APPLICATION NUMBER:
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                                                                    TYPE: DNA
ORGANISM: Mouse
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                                                                                                             ID NO 230
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               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JE OF INVENTION: Compositions Isolated From Skin Cells OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230, Apr
                                                                                                                                                                                                                                                                                                                                                                                                  995 GCTACAGCCAGGACAACGA 1013
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 l Similarity 84.:
16; Conservative
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                                                                                               2004
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                                                                                                                                                                                                                                                                                                                                                                                                                            GGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
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Sleeman, Matthew
Onrust, Rene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watson, James D.
                                                                                                                                                                                                                                               Strachan, Lorna
Sleeman, Matthew
Onrust, Rene
                                                                                                                                                                                                                                                                                                                               Application US/09312283C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                      Krishanand D.
                                                                                                                                                                                           and Methods for Their Use
                                                                                                                                                                                                                                    James G
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            79.0%;
84.2%;
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84.2%;
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78.9%;
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Pred. No. 4e
Score 15.8; DB 3;
Pred. No. 4e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4e+
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Pred. No. 4
                                                                                                                                                                                                      Isolated from Skin Cells
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                         Length 2004;
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US-09-949-016-13629
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                                                                      Query Match
                                                                                                                                                                                                                                            SEQ ID NO 13629
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                                                                                                        09-949-016-13629
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                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: US 6

PRIOR APPLICATION NUMBER: US 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                      OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                              OFTWARE:
                                                                                                                                                                                                                                                                              UMBER OF SEQ ID NOS:
                                                                                                                                        OCATION:
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                                                    Local
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                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 AGCTACAGCCTGGACTACG 698
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                                  l Similarity
16; Conserv
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GGUACAGCCAGGACUACGA 20
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                                    Conservative
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH HUMAN DISEASE,
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                                                  84.2%;
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78.9%;
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                                                                                                                                                                                                                                                          Version 4.0
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                                                  Score 15.8;
Pred. No. 4
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Pred. No. 4
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US-09-252-991A-15933
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US-10-200-012-5
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                                                                                         RESULT 20
US-07-925-695-6/c
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 15933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Huang, Shi PR/SET- Domain Containing Nucleic Acids,
TITLE OF INVENTION: PR/SET- Domain Containing Nucleic Acids,
TITLE OF INVENTION: Polypeptides, Antibodies and Methods of Use
FILE REFERENCE: P-LJ 5301
CURRENT APPLICATION NUMBER: US/10/200,012
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 09/910,478
PRIOR APPLICATION NUMBER: US 09/910,478
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.0%;
Best Local Similarity 88.2%;
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
                                                  Sequence 6, Application US/07925695
Patent No. 5428145
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                             Best Local
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                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 249
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (250)...(1761)
                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
APPLICANT:
APPLICANT:
                                                                                                                                                                 1001 GGTACAGCGAGGACTAC 1017
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 OKAMOTO, Hiroaki
NAKAMURA, Tetsuo
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                                                                                                                                                                                                                                                           77.0%;
82.4%;
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Pred. No. 5.9e+02;
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Pred. No. 6.2e+02;
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Best Local Similarity
""" has 14; Conserve
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US-07-925-695-7/c
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PRIOR APPLICATION DATA:
APPLICATION UMMER: JP 287402/91
APPLICATION UMMER: JP 287402/91
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 360441/91
APPLICATION NUMBER: JP 360441/91
PILING DATE: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/07925695
Patent No. 5428145
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INFORMATION FOR SEQ ID NO: 6:
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APPLICANT: OKAMOTO, Hiroaki
APPLICANT: NAKAMURA, Tetsuo
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TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/87-48009
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 199208
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                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                             STREET:
                                                                      ZIP: 20036
                                                                                           COUNTRY:
                                                                                                                                                                ADDRESSEE: Beveridge,
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1850 M Street, N.W., Suite 800
                                                                                                                                                 1850 M Street, N.W., Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659-2811
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73.7%;
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                                                                                                                                                                                                                                                                           Tetsuo
                                                                                                                                                    DeGrandi, Weilacher & Young
, N.W., Suite 800
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Pred. No. 6.4e+02;
3; Mismatches 2;
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CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.25

US/07/925,695

APPLICATION NUMBER:

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RESULT 23
US-09-949-016-12106
; Sequence 12106, Application US/09949016
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US-09-949-016-17037
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                                                                                                                                                                                                                        ORGANISM: Human
JS-09-949-016-17037
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: WUI 64470
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                      Local Similarity 82.4 es 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weilacher, Robert G. REGISTRATION NUMBER: 20,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 09-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                    NT FILING DATE: 2000-04-14
APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/237,768
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FastSEQ for Windows Version 4.0
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                                                                                      AGGTAGAGCCAGGACTA 105695
                                                                                                                     AGGUACAGCCAGGACUA 17
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ilarity 73.7%;
Conservative
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82.4%;
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                                                                                                                                                                    Score 15.4; DB 3
Pred. No. 6.6e+02
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Pred. No. 6.
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RESULT 25 US-09-105-390-33

33, Application US/09105390

Patent No.

GENERAL INFORMATION:
APPLICANT: Rodrigue
TITLE OF INVENTION:
TITLE OF INVENTION:

Rodriguez, Raymond VENTION: Rice Beta-Glucanase Enzymes VENTION: and Genes

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RESULT 24
US-09-252-991A-15084
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                                                                Matches
                                                                                                  Query Match
                                                                                                                                                                                               SEQ ID NO 15084
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                                                                                                                                   -09-252-991A-15084
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                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE TILE REPERSENT.
                                                                                                                                              TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION NUMBER: 60/241,755
RRIOR FILING DATE: 2000-10-20
RRIOR APPLICATION NUMBER: 60/237,768
RIOR FILING DATE: 2000-10-03
RRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                   ENGTH:
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                                                                                  Local
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353 AGCTACCGCCAGGACGACGA 372
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                               1 AGGUACAGCCAGGACUACGA 20
                                                                l Similarity
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                                                                                                                                                                                                                                                                                                                                      107196.136
                                                                                                                                                                                                                                                                                                                                                    Rubenfield et al.

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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PRR: US 60/074,788
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82.4%;
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                                                                              76.0%;
                                                                              Score 15.2;
Pred. No. 7.4
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Pred. No. 6
                                                                Mismatches
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                                                                                                DB 3; Length 546;
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STREET:

Palo Alto

350 Cambridge Ave., Suite 250

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USA

ZIP: 94306

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RESULT 26
US-09-270-767-10699/c
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                                                                                                                                    ; ORGANISM: Drosophila melanogaster US-09-270-767-10699
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                                                                                                                                                                                                  Sequence 10699, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10699
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Best Local S
                                                                   Matches
                                                                                                  Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 924 base pairs
                                                                                                                                                                      LENGTH: 987
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-JUN-97
ATTORNBY/AGENT INFORMATION:
NAME: PELITHORY, JOANNE R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 85.0
                                                                            Match 76.0%;
Local Similarity 80.0%;
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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650
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                                1 AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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AGGGACAGGGAGGACTACGA 631
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                                                                    Conservative
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85.0%;
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Pred. No. 7.5e
0; Mismatches
                                                                 Score 15.2; DB 3; Length 987; Pred. No. 7.5e+02; Indels
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7.5e+02;
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RESULT 28
US-09-270-767-20078
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; ORGANISM: Drosophila melanogaster
US-09-270-767-4796
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Patent No. 6703491

GRUSRAL INFORMATION:

APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4796
                                                                                                                                                                                                                                                                                                         US-09-105-390-49
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Matches
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SEQ ID NO 20078
LENGTH: 1029
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1029
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                           NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%;
Local Similarity 80.0%;
les 16; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 16; Conserv
                                                                                                          STREET: 350 Camb
CITY: Palo Alto
                                                       ZIP: 94306
                                                                  COUNTRY:
                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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                                                                                           ß
                                                                                                                            350 Cambridge Ave., Suite 250
                                                                        USA
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Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.2; DB 3;
Pred. No. 7.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
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IBM Compatible

CURRENT APPLICATION DATA:

FastSEQ for Windows Version 2.0

OPERATING SYSTEM:

APPLICATION NUMBER:

Filed herewith

US/09/105,390

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RESULT 31
US-09-252-991A-14538/c
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US-09-252-991A-14826
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Sequence 14538, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity Matches 17; Conserv
                                                                                                                                                          Matches
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                  SEQ ID NO 14826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                      -09-252-991A-14826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-(
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      ENGTH: 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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                                                                                                                         1 AGGUACAGCCAGGACUACGA 20
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                                                                                                                                                                       Similarity
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                                                                                           AGCTACCGCCAGGACGACGA 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09252991A
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1...1035
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1998-02-18
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85.0%;
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                                                                                                                                                                    76.0%;
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                                                                                                                                                       Score 15.2; DB 3;
Pred. No. 7.6e+02;
1; Mismatches
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Pred. No. 7.5e+02
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                                                                                                                                                                                     DB 3; Length 1521;
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US-09-105-390-1
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US-09-105-390-1
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SEQ ID NO 14538
LENGTH: 1596
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APPLICANT: Marc J.
                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Marc J. Rubenfield et al.
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base pair
                                                                                                                                                                            NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                      FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94306
                                                                                                                                             TELEFAX: 650-324-0960
                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60 FILING DATE: 25-JUN-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                             : 2230 base pairs nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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               linear
                                                                                                                                                                650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                    Filed herewith
                                 single
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1998-02-18
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                                                                                                                                                                                                                                                                                            60/050,675
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Query Match Best Local Similarity

76.0%; 85.0%;

Score 15.2; Pred. No. 7

DB 3; .7e+02;

Length 2230;

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US-09-949-016-13044
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; LOCATION: (1)...(9319)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                               ; ORGANISM: Human
US-09-949-016-14958
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SEQ ID NO 13044
LENGTH: 9319
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
Query Match
Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14958
LENGTH: 23406
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 207012
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                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 76.0%;
Local Similarity 75.0%;
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                    76.0%;
80.0%;
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  Score 15.2; DB 3;
Pred. No. 8.1e+02;
1; Mismatches 3;
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Pred. No. 7.9e+02;
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                                             Length 23406;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
TITLE OF INVENTION NUMBER: US/09/949,016.
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,758
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
; ORGANISM: Human
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(30456)
; OTHER INFORMATION: n = A
US-09-949-016-14213
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US-09-949-016-15248
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; Sequence 14213, Application US/09949016
; Patent No. 6812339
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FURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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SEQ ID NO 15248
LENGTH: 28283
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(28283
OTHER INFORMATION: n =
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                                                                                                                                                 TYPE: DNA
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80.0%;
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RESULT 38
US-09-949-016-11995/c
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                                                                                                          SEQ ID NO 11995
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                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INFORMATION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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ITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-20
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                                                      ORGANISM: Human
                                                                                     ENGTH:
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APPLICATION NUMBER: 60/231,498
FILING DATE: 2000-09-08
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75.0%;
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Pred. No. 8.
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Pred. No. 8
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DB 3;
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Query Match

76.0%; Score 15.2;

Length 60304;

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US-09-949-016-17264/c
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Query Match
Best Local Similarity
                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12361
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                                                    NAME/KBY: misc feature
LOCATION: (1)...(69874)
OTHER INFORMATION: n = A,T,C or G
-09-949-016-12361
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                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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IITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
IITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                     ORGANISM: Human
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   Score 15.2;
Pred. No. 8.
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Pred. No. 8.2e+02
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   DB 3;
                     Length 69874;
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RESULT 41
US-09-949-016-13049/c
; Sequence 13049, App
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LOCATION: (1)...(69874);
COTHER INFORMATION: n = A,T,C or G
US-09-949-016-13049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 42
US-09-750-580-1/c
                                                                                                                                         APPLICANT: EDbets-Reed, Dana
APPLICANT: Saltes-Cid, Luisa
APPLICANT: Saltes-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITION
FILE REFERENCE: 89.US2.CIP
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
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SEQ ID NO 13049
LENGTH: 69874
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09750580 Patent No. 6455280 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001307
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               PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-1 PRIOR APPLICATION NUMBER:
                                                                                       PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB00/0101
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/IB99/02058
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                                                                       PRIOR FILING DATE:
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 FILING DATE:
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Similarity 80.0%;
16; Conservative
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Ebbets-Reed, Dana
Salter-Cid, Luisa
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89.US2.CIP
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             1999-12-20
NUMBER: US 49/469/099
1999-12-21
NUMBER: US 60/113,686
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1998-12-22
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Pred. No. 8.2e
1; Mismatches
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PRIOR FILLMG DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTMARE: Patent.pm
SEQ ID NO 1
                           NAME/KBY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.rp
NAME/KBY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
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LOCATION: 10946..12946
OTHER_INFORMATION: 5'regulatory region
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OTHER INFORMATION: exon
NAME/KEY: exon
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OTHER INFORMATION: exon
NAME/KEY: exon
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OTHER INFORMATION:
NAME/KEY: allele
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LOCATION: 1427
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LOCATION: 14992..15012
OTHER_INFORMATION: 17-41.pu
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OTHER INFORMATION:
NAME/KEY: allele
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                                                                                                                                                       OTHER INFORMATION: 17-41.rp complement NAME/KEY: primer_bind LOCATION: 42070..42090
                                                                                                                                                                                                                                                                                                                                NAME/KEY: primer_bind
LOCATION: 12581..1260
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
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LOCATION: 1357..1377
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LOCATION: 15460..15482
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OTHER INFORMATION: 17-42.rp complement
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                                                                                                                                       OTHER INFORMATION: 20-841.pu
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           primer_bind
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Best Local S
Matches 15
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NAME/KEY: misc_binding
LOCATION: 77046..77070
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65250 AGGTAAAGCCAGGAATAAGA 65231
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77039..77057
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75.0%;
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Pred. No. 8
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                                                                 Mismatches
                                                                                  8.2e+02
                                                                                                  DB 3;
                                                                                              Length 81001;
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39701 AGGCACAGCCAGGACTCAGA 39682

RESULT 45 US-09-949-016-14883/c

Sequence 14883, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:

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                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14882
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US-09-949-016-14881/c
                                                  Query Match
Best Local Similarity
                                                                                                                                                                               SEQ ID NO 14882
                                   Matches
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SEQ ID NO 14881
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APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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HITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
HITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                           LENGTH: 146307
                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 16; Conserv
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                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                    FILING DATE:
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                                   16; Conservative
1 AGGUACAGCCAGGACUACGA 20
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llarity 80.0%;
Conservative
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Pred. No. 8.2e
1; Mismatches
                                                    Score 15.2;
Pred. No. 8
                                   Mismatches
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OF DETECTION AND USES THEREOF
                                                                 Length 146307;
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US-09-949-016-14883
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US-09-949-016-14884/c
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                                                                                                                                                                          RESULT 47
US-09-949-016-14885/c
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US-09-949-016-14884
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Patent No. 6812339
GENERAL INFORMATION:
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LENGTH: 146307
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14884
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
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CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                           Sequence 14885, Application US/09949016
Patent No. 6812339
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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80.0%;
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Pred. No. 8.2e+02;
1; Mismatches 3;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT ETLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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US-09-949-016-14885
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; Sequence 14887, Application US/09949016
; Patent No. 6812339
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US-09-949-016-14886
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14885
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERBOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THERBOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-01-0-3

PRIOR FILING DATE: 2000-01-0-3

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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SEQ ID NO 14886
LENGTH: 146307
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
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RESULT 50
US-09-949-016-14888/c
; Sequence 14888, Application US/09949016
parent No. 6812339
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; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-14887
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Search completed: March 18, 2006, 18:40:11 Job time : 103.538 secs
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity 80.0
Matches 16; Conservative
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-09-949-016-14888
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                          39701 AGGCACAGCCAGGACTCAGA 39682
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39701 AGGCACAGCCAGGACTCAGA 39682
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Pred. No. 8.2e+02;
1; Mismatches 3
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Result
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Maximum Match 100%
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APPLICANT: Weiner, George
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
TITLE OF INVENTION: Cell Lysis and Treating Cancer
FILS REFERENCE: C1039/7052 (AWS)
CURRENT APPLICATION NUMBER: US/09/888,326
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,346
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 68
LENGTH: 20
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; Sequence 68, Application US/09888326
; Publication No. US20030026801A1
                                                 RESULT 2
US-09-776-479-391
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Sequence 391, Application US/09776479
Publication No. US20030087848A1
GENERAL INFORMATION:
APPLICANT: Bratzler, Robert L.
APPLICANT: Petersen, Deanna M.
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Best Local S
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981
982
                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
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1 AGGTACAGCCAGGACTACGA 20
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US-10-425-115-19790
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US-10-950-009-169
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US-10-950-009-169
US-10-950-009-191908
US-10-79-543-15178
US-09-925-065A-855911
US-10-799-543-13240
US-10-799-543-13240
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US-09-98-168-995-1579
US-09-98-168-995-13974
US-09-98-157-5119
US-09-96-157-10356
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US-10-764-324-3876
US-10-424-599-9946
US-10-029-386-27061
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Pred. No. 3
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19742, A
16309, A
169, App
40113, A
1908, Ap
1908, Ap
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9946, Ap
27061, A
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31568, A

16178, A

43280, A

15779, A

6132, Ap

4406, A

5119, Ap

10354, Ap
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13240, A
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APPLICANT: Pouron, Yves
IITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
IITLE OF INVENTION: Treatment of Asthma and Allergy
ITLE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOFTMARE: PRESENCE for Windows Version 3.0
SEQ ID NO 391
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Petersen, Robert L.
APPLICANT: Petersen, Deanna M.
APPLICANT: Petersen, Vee
ITILE OF INVENTION: Immunostimulatory Nucleic Acids for the
ITILE OF INVENTION: Treatment of Asthma and Allergy
ITILE REFERENCE: C1037/7013 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/09/776,479
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR APPLICATION NUMBER: US 60/179,991
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 1093
SOPTWARE: FastSEQ for Windows Version 3.0
LENGTH: 20
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                                                                                                                                  RESULT 4
US-10-112-653-379
IS-10-112-653-379
; Sequence 379, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
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US-09-776-479-391
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                APPLICANT: Krieg, Arthur M.
APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
FILE REFERENCE: C01039/70060 (AWS)
CURRENT APPLICATION NUMBER: US/10/112,653
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Pred. No. 3.
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Pred. No. 3
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Best Local Similarity 90.0
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LENGTH: 20
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                                                                                                                                  APPLICANT: Schetter, Christian
APPLICANT: Vollmer, Jorg
TITLE OF INVENTION: Immunostimulatory Nucleic Acids
FILE REFERENCE: C1039/7035 (HCL/MAT)
CURRENT APPLICATION NUMBER: US/10/314,578
CURRENT FILING DATE: 2002-12-09
                                                                                                                                                                                                                                                               SENERAL INFORMATION:
                                                                  PRIOR APPLICATION NUMBER: US 60/156,135 PRIOR FILING DATE: 1999-09-27
                                                                                                       PRIOR APPLICATION NUMBER: US 60/156,113 PRIOR FILING DATE: 1999-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids FILE REPERENCE: C1037/7025 (HCLMAT)
CURRENT APPLICATION NUMBER: US/10/017,995
CURRENT FILING DATE: 2001-12-18
                   NUMBER OF SEQ ID NOS:
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ORGANISM: Artificial Sequence
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5. US20030212026A1
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Windows Version 3.0
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Pred. No.
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LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: MARSHALL, WILLIAM B.
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Best Local Similarity
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                                                                                                 PRIOR APPLICATION NUMBER: 09/193,653
PRIOR PILLING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 08/739,264
PRIOR FILING DATE: 1996-10-29
                                                                                                                                                                                                                        FILE REFERENCE: P01936US06
CURRENT APPLICATION NUMBER: US/10/800,926
CURRENT FILING DATE: 2004-03-15
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CURRENT FILING DATE: 2004-04-23
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/883,550 PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: OLIGORIBONUCLEOTIDES ALERT THE IMMUNE SYSTEM OF ANIMALS TITLE OF INVENTION: TO THE IMMINENCE OF MICROBIAL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the TITLE OF INVENTION: Treatment of Asthma and Allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bratzler, Robert L. APPLICANT: Petersen, Deanna M.
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Local Similarity 90.0%;
                                                                                APPLICATION NUMBER: 08/517,016
                                        APPLICATION NUMBER:
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No. US20050032731A1
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                                                                                                                                            ; OTHER INFORMATION: Genbank Accession No. AB012214 US-10-152-319A-532
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SOFTWARE: PatentIn Ver.
SEQ ID NO 3
                                                                                                                                                                                                                                Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 2221
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 532
LENGTH: 5253
                                                                   Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
                                                                                                     Query Match
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PRIOR PRILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Higgs, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
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PRIOR FILING DATE: 2001-06-19
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                                                                                                                                                                                 TYPE: DNA
ORGANISM: Rattus norvegicus
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/324,928 FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/303,808 FILING DATE: 2001-07-10
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APPLICATION NUMBER: US 60/330,462
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2679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/303,807
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GGTACAGCCAGGACTACG 2696
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o. US20040072160A1
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                                                                     2.
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Pred. No.
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                                                                                                        DB 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                        Length 5253;
                                                                     Indels
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                                                                     Gaps
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FILE REFERENCE: 38-21 (5322)B

FULE REFERENCE: 38-21 (5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 14343

LENGTH: 281
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US-09-925-065A-693333/c
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US-10-425-115-14343
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                                                                                                                                                               ; ORGANISM: Homo sapiens 
US-09-925-065A-693333
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PRIOR PRILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14343, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69333, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
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                                                                                                                                                                                                                                             SEQ ID NO 693333
                                                                                Matches
                                                                                                     Best Local
                                                                                                                      Query Match
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: MRT4577_113070C.1
                                                                                                                                                                                                                          LENGTH: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y match
Local Similarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 AGGTACAGCCAGATCTACGA 179
398 AGGCACAGCCAGGACTAAGA 379
                                                                                17;
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                                      1 AGGUACAGCCAGGACUACGA 20
                                                                                                   Similarity
                                                                                Conservative
                                                                                                 84.0%;
85.0%;
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Pred. No. 1.3e+02;
2; Mismatches 2;
                                                                                                     Score 16.8;
Pred. No. 1.
                                                                                  Mismatches
                                                                                                     1.3e+02;
                                                                                                                           DB 4;
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RESULT 14
US-10-653-047-3156
; Sequence 3156, Application US/10653047
; Publication No. US20040229367A1
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; ORGANISM: Homo sapiens
US-09-925-065A-73830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-322-281-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 33, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                               Matches
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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CURRENT FILING DATE: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David W. APPLICANT: Marc S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/252,147
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                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (1)...(145068)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence 73830, Application US/09925065A blication No. US20050228172A9
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION: Novel Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                      50545
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FILING DATE: 2001-01-16
APPLICATION NUMBER: US 60/289,846
FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2000-11-20
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                                                                                                                      AGGTACTGCCAGGACCACGA 50564
                                                                                                                                               AGGUACAGCCAGGACUACGA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marc S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10322281
No. US20040126762A1
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                                                                                                                                                                                                            Score 16.8; DB 7
Pred. No. 1.1e+02
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Pred. No. 1
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                                                                                                                                                       ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-925-065A-369463
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US-09-925-065A-369463
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; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-653-047-3156
                                                                                                                                                                                                                                        SEQ ID NO 369463
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Best Local Similarity
Matches 15; Conser
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LENGTH: 246
                                                                                                                 Query Match
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                                                                              Matches
                                                                                                 Best Local
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                                                                                                                                                                                                                                                      PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SOPTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: US/09/533,559
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Randy M. APPLICANT: Michael
                                                                                                                                                                                                                                                                                                                                                                              RIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE:
                                                                                                                                                                                                                 LENGTH: 586
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                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-16
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  39
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                                   1 AGGUACAGCCAGGACUAC 18
                                                                                                 Similarity
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Jeffrey R.Shuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peter Bjarke Olsen
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Ib Groth Clausen
                                                                                Conservative
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                                                                                                                                                                                                                                                        for Windows Version 4.0
                                                                                                                                                                                                                                                                                              2001-05-09
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                                                                                                 82.0%;
83.3%;
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83.3%;
56
                                                                                                 Score 16.4;
Pred. No. 2.
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Pred. No. 2.
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2.1e+02;
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                                                                                                                    Length 586;
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RESULT 16 US-10-425-114-8343

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APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven B

APPLICANT: Tabaska, Jack B

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 36-21 (5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 8343

LENGTH: 1308

TYPE: DNA
                                                                                                          RESULT 18
US-09-997-722-199
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TITLE OF INVENTION: NOVEL COMPOSITIONS AND ME
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.29452000128
CURRENT APPLICATION NUMBER: US/10/034,650
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 09/474,377
PRIOR PILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 17
                                                                                                                                                                                                                                                                                                                                              US-10-034-650-1
                                                   Sequence 199, Application US/09997722 Publication No. US20040072154A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Fast:
SEQ ID NO 1
LENGTH: 31632
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Clone ID: 700748540_FLI
-10-425-114-8343
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Morris, David
APPLICANT: Engelhard, E
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                                                                                        26940 AGGTACAGCCAGGGCTAC 26923
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83.3%;
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83.3%;
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                                                                                                                                                                                                                                                             Score 16.4; DB 6;
Pred. No. 1.9e+02;
2; Mismatches 1;
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Pred. No. 2
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; FEATURE:
, NAME/KEY: variation
; LOCATION: (1)...(168749)
; OTHER INFORMATION: n = at
US-10-085-117-250
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US-10-085-117-250
Query Match
Best Local Similarity 83.3
Conservative
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APPLICANT: MOITIS, David W.
APPLICANT: MOITIS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 199
LENGTH: 96599
                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 250
LENGTH: 168749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 250, A Publication No.
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NAME/KEY: misc feature
LOCATION: (4189).. (4208)
OTHER INFORMATION: "n" at p
FEATURE:
FEATURE:
NAME/KEY: misc feature
LOCATION: (9552).. (10001)
OTHER INFORMATION: "n" at p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (88386)..(88405)
OTHER INFORMATION: "n" at positions 88386 through 88405 can be any base.
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LOCATION: (54062)..(54139)
OTHER_INFORMATION: "n" at positions 54062 through 54139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (27805)..(27824)
OTHER INFORMATION: "n" at positions 27805 through 27824 can
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                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                  TYPE: DNA
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o. US20030232334A1
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83.3%;
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                                   Score 16.4; DB 6
Pred. No. 1.8e+02
                    Mismatches
                                                          DB 6;
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US-11-097-143-27752
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Best Local
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
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                                                             PRIOR FILING DATE: 1999-10-19
                                                                                                                          PRIOR APPLICATION NUMBER: 60/157,832
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ITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
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                                                                                 APPLICATION NUMBER: 60/160,191
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                                                                                                                                                APPLICATION NUMBER: US/11/097,143 FILING DATE: 2005-04-04
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CATION NUMBER: 60/164,769
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US20050208558A1
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                                       60/161,932
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                                                                                                                                                                                                                                SEQ ID NO 27751
                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
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Publication No. US20050208558A1
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CURRENT FILING DATE: 2005-04-04
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                                                                                                                                                                                            TYPE: DNA
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THE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/164,769 FILING DATE: 1999-11-12
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2160 GTÁCAGCCAGGACTÁC 2145
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                                  GUACAGCCAGGACUAC 18
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87.5%;
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                                                                                             Score 16;
Pred. No.
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US-11-097-143-12094/c ; Sequence 12094, Application US/11097143

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SEQ ID NO 85
LENGIH: 96600
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PRIOR
                                                 PEATURE: Misc feature LOCATION: (7789)..(7808) OTHER INFORMATION: "n" at FEATURE:
                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
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CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Morris, David
APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71171/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/161,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: DROSOPHILA
                 NAME/KEY: misc feature LOCATION: (9978)..(999
                                                                                                                                            TYPE: DNA
ORGANISM: Mus musculus
LOCATION: (9978)..(9997)
OTHER INFORMATION: "n" a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-11-12
APPLICATION NUMBER: 60/173,383
FILING DATE: 1999-12-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-10-28
APPLICATION NUMBER: 60/164,769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/191,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-01-12
APPLICATION NUMBER: 60/184,831
FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2160
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GTACAGCCAGGACTAC 2145
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No. US20040072154A1
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positions
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Pred. No.
                                                                        7789
9978 through
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EXPRESSION O
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US-10-624-149A-2/c
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                                                                  Sequence 2, Application US/10624149A
Publication No. US20040109873A1
GENERAL INFORMATION:
APPLICANT: Neubauer, Antonie
APPLICANT: Ziegler, Christina
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                             Query Match
APPLICANT: Ziegler, Christina
TITLE OF INVENTION: gM-Negative EHV-Mutants without Heterologous
FILE REFERENCE: 1/1372
CURRENT APPLICATION NUMBER: US/10/624,149A
CURRENT FILING DATE: 2003-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (20780)..(20
OTHER INFORMATION: "n"
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LOCATION: (27797)...(27816)
OTHER INFORMATION: "n" at
FEATURE:
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LOCATION: (14125)..(14144)
OTHER INFORMATION: "n" at
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LOCATION: (63387)..(63406)
OTHER INFORMATION: "n" at positions 63387 through 63406
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LOCATION: (33786)..(33805)
OTHER INFORMATION: "n" at
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LOCATION: (31149)..(31
OTHER INFORMATION: "n"
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LOCATION: (60915)..(60934)
OTHER INFORMATION: "n" at
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LOCATION: (45961)..(45980)
OTHER_INFORMATION: "n" at
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LOCATION: (34873)..(34892)
OTHER INFORMATION: "n" at positions 34873 through
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (57012)..(57031)
OTHER INFORMATION: "n" at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (55271)..(55
OTHER INFORMATION: "n"
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                                                                                                                                                                                                                                                                               Match 80.0%;
Local Similarity 87.5%;
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91766 GTACAGCCAGGACTAC 91781
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"n" at ]
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*n" at ]
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"n" at ]
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"n" at ]
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Pred. No. 2.9e+02
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PRIOR APPLICATION NUMBER: 60/403,282

2002-08-

APPLICATION NUMBER: DE 10317008 APPLICATION NUMBER: DE 10233064

2002-07-2003-04-11

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Matches
                                                                     Query Match
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                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-132060
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                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DATABASE ACCESSION NUMBER: NC 001844, NCBI
DATABASE ENTRY DATE: 2000-08-01
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JBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UTHORS: Telford, E.A.
UTHORS: Watson, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sence 132060, Application US/09925065A
lication No. US20050228172A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THORS: Cullinane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/289,846 FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DNA sequence of equine herpesvirus-4 L: J. Gen. Virol.
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                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Davison, A.J.
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GGUAÇAGÇÇAGGAÇUAÇGA 20
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                                                79.0%;
78.9%;
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                                                    Score 15.8;
Pred. No. 4
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Pred. No.
                                   Mismatches
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                                                    .3e+02
                                                                       DB 4;
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                                                                   ; ORGANISM: Homo sapiens
US-09-925-065A-290636
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US-09-925-065A-290636/c
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                                                                                                                                                             SEQ ID NO 290636
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/925,065A
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ITLE OF INVENTION: Identification and Mapping of Single
ITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
Local Similarity
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                                                                                                                                                                                                                                               FILING DATE: 2001-01-16
APPLICATION NUMBER: US 60/289,846
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78.9%;
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78.9%;
                                                                                                                                                                                     Version 4.0
Score 15.8;
Pred. No. 4
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Pred. No. 4
.2e+02
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                Length 533;
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US-10-357-930-15913/c
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; LOCATION: 502, 516, 518, 525
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-15913
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PRIOR FILLING DATE: 2003-02-16
PRIOR FILLING DATE: 2000-02-17
PRIOR FILLING DATE: 2000-02-17
PRIOR PILLING DATE: 2000-02-17
PRIOR PILLING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILLING DATE: 2000-05-25
PRIOR PILLING DATE: 2000-06-9
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILLING DATE: 2000-06-9
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
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US-09-925-065A-813093
               CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
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                                                                                                                                                                                                                                       Sequence 813093, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 15913
LENGTH: 542
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Best Local Similarity
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APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007ECN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
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FILING DATE: 2001-01-16
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78.9%;
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Pred. No. 4.2e+02;
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APPLICATI: MONAHAN, John
TITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT PILING DATE: 2003-02-04
PRIOR REPLICATION NUMBER: 09/785,276
PRIOR PELILING DATE: 2003-02-16
PRIOR PRILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR PILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR PILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PILING DATE: 2000-12-13
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; ORGANISM: Homo sapiens
US-09-925-065A-813093
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                                                                                                                                                         RESULT 32
US-10-767-701-25552
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US-10-357-930-45741
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 813093
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Best Local Similarity 84.2%;
                                                                                 Sequence 25552, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 45741
LENGTH: 592
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version
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122 GGCACAGCCAGGACTAAGA 140
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78.9%;
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Pred. No. 4.2e+02;
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Pred. No. 4
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Best Local
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Best Local
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Publication No. US20040214272A1
                                                             APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C193/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
                                                CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 369326
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DIHER INFORMATION:
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lication No. US20050196754A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 59643
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NUMBER: 09/540,217
: 2000-03-31
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89.5%;
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Pred. No. 4.2e.
0; Mismatches
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Pred. No. 4
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; ORGANISM: Human
US-10-027-632-113386
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                                                                                        Query Match
Best Local
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 113386
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 108827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 113386, Application US/10027632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        URRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OFTWARE: Cust
                                                                                                                                                                                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Wang, David G.
ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-03-29
451 GGCACAGCCAGGACTAAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                               LING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                          LING DATE: 2000-02-24
                                                                     l Similarity
16; Conserv
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                                GGUACAGCCAGGACUACGA 20
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                                                                       Conservative
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binding protein (phnK), accession number J05260, Smith-Waterman Sco
=528.
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                                                                                      84.2%;
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Pred. No. 4
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                                                                                        2e+02;
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                                                                                                       Length 752;
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                                                                   Indels
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RESULT 36 US-10-027-632-113387/c

Sequence 113387, Application US/10027632 Publication No. US20020198371A1

PELICANT: Wang, David G. ITLE OF INVENTION: Identification and Mapping of Single Nucleotide Ś

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US-10-027-632-113387
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                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PELICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-02-34
PRIOR PELING DATE: 2000-02-34
PRIOR PELING DATE: 1999-01-23
PRIOR PELING DATE: 1999-01-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-113386
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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LENGTH: 752
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 113386
LENGTH: 752
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
                                             Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                     Matches
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23 APPLICATION NUMBER: US 60/156,358
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APPLICATION NUMBER: US 60/146,002
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84.2%; Pred. No. 4.2e+02;
                        79.0%; Score 15.8; DB 6; 84.2%; Pred. No. 4.2e+02; tive 1; Mismatches 2;
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                             Indels
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US-10-027-632-113387/c
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; ORGANISM: Human
US-10-027-632-113387
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CURRENT PILLING DATE: US/11/097,143
CURRENT FILLING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILLING DATE: 1999-10-05
PRIOR PILLING DATE: 1999-10-19
PRIOR PPLICATION NUMBER: 60/160,191
PRIOR PPLICATION NUMBER: 60/161,932
PRIOR PPLICATION NUMBER: 60/161,932
PRIOR PILLING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILLING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILLING DATE: 1999-11-28
PRIOR PILLING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILLING DATE: 1900-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 113387 LENGTH: 752
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 GGCACAGCCAGGACTAAGA 433
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Pred. No. 4.
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4.2e+02;
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Length 752;

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NUCLEIC ACID EXPRESSION OF 10,000 OR MORE

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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-10-389-647-172
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                                                                                                                  FILE REFERENCE: 11000.1011c4U
                                                                                                                               TITLE OF INVENTION: Compositions TITLE OF INVENTION: and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/389,647
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                                                                                                                                                                    PPLICANT:
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHICANT: SCHUSTER, Martin
PHICANT: LOSTROH, Candi
TILE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
              ID NO 18
ENGTH: 1057
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                                                                                                                                                                                                                                                                                                                                                                                       166 AGCTACAGCCTGGACTACG 184
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                                               FastSEQ for Windows Version 4.0
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                                                                                                                                                       Murison, James G.
Kumble, Krishanand D.
                                                                                                                                                                                                  Onrust, Rene
                                                                                                                                                                                                                Strachan, Lorna
Sleeman, Matthew
                                                                                                                                                                                                                                                                                                    Application US/09866050A
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o. US20040033549A1
                                                                                                 CATION NUMBER: US/09/866,050A
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                                                                                                                                                                                                                                                     James D.
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                                                                                                                                and Methods for Their Use
                                                                               2001-05-24
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78.9%;
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Pred. No. 4.2e+02;
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Pred. No. 4
                                                                                                                                                Isolated From Skin Cells
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RESULT 43
US-09-866-050A-447
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                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Rat
US-10-152-661-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Rat
US-09-866-050A-18
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                                                                                                                                                          Sequence 447, A Publication No.
                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                       APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/866,050 PRIOR FILING DATE: 2001-05-24 PRIOR APPLICATION NUMBER: 60/221,232 PRIOR FILING DATE: 2000-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/206,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 11000.1011c5
ITLE OF INVENTION: Compositions Isolated From Skin Cells ITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/069,726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/188,930
                                                                                                                                                                                                                                                           1022 GCTACAGCCAGGACAACGA 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-05-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/NZ99/00051
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                                                                                  Strachan, Lorna
Sleeman, Matthew
                                                                       Onrust, Rene
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Sleeman, Matthew
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No. US20030022835A1
                                                                                                                                                          Application US/09866050A o. US20030040471A1
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                    Krishanand D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions
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                                                       James G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            James G
                                                                                                                                                                                                                                                                                                                                                        79.0%;
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84.2%;
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Pred. No. 4.
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                                                                                                                                                                                                                                                                                                                                                                     Length 1057;
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APPLICANT: MUTISON, James G.
APPLICANT: KUMISON, James G.
APPLICANT: KUMISON, James G.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR APPLICATION NUMBER: 09/1312,283
PRIOR APPLICATION NUMBER: 09/132,283
PRIOR APPLICATION NUMBER: 09/188,930
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US-10-152-661-447
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                                         RESULT 45
US-09-866-050A-230
yS-09-866-050A-230
ySequence 230, Application US/09866050A
publication No. US20030040471A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Rat
US-10-152-661-447
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CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1890
TYPE: DNA
ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                            Query Match 79.0%;
Best Local Similarity 84.2%;
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Watson, James D.
APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/069,726 PRIOR FILING DATE: 1998-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1890
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Local Similarity 84.2%;
hes 16; Conservative
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Sleeman, Matthew
Onrust, Rene
                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 4.1e+02;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                 Score 15.8; DB 5;
Pred. No. 4.1e+02;
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APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Sk
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866;050A
CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 230
LENGTH: 2004
                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Compositions isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c5
CURRENT FILING DATE: 1000-05-20
PRIOR APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: FCT/NZ99/00051
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR PRICING DATE: 1998-11-09
PRIOR PRICING DATE: 1998-11-09
PRIOR PRICING DATE: 1998-11-09
PRIOR PRICING DATE: 1998-11-09
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; ORGANISM: Rat
US-09-866-050A-230
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US-10-152-661-230
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                                    S
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; ORGANISM: Rat
US-10-152-661-230
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Best Local Similarity 84:2
Matches 16; Conservative
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Publication No. US20030022835A1
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APPLICANT:
APPLICANT:
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APPLICANT:
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SEQ ID NO 230
                                                                                   Matches
                                                                                                    Query Match
Best Local
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                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-04-29
                                                                                                                                                                                                                            LENGTH:
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  995 GCTACAGCCAGGACAACGA 1013
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                                                                                   16;
                                        2 GGUACAGCCAGGACUACGA 20
                                                                                                        Similarity
                                                                                                                                                                                                                                                                       FastSEQ
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Sleeman, Matthew
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Onrust, Rene
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                                                                                   Conservative
                                                                                                                                                                                                                                                                       for Windows Version 4.0
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84.2%;
                                                                                                        79.0%;
84.2%;
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Pred. No. 4.1e+02
                                                                                   1; Mismatches
                                                                                                        Score 15.8;
Pred. No. 4.
                                                                                                           4.1e+02;
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                                                                                            Indels
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US-10-027-632-101774

Query Match:

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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 101774, Application US/10027632 blication No. US20030204075A9
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ublication No. US20020198371A1
)RGANISM: Human
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                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/198,676
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                                                                                                                                                                   TILING DATE: 2000-02-24

EPLICATION NUMBER: US 60/167,363

TILING DATE: 1999-11-23

PPLICATION NUMBER: US 60/156,358

FILING DATE: 1999-09-28
                                                                                                                                                       PLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                        PLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                   LING DATE: 2000-03-29
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; TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      URRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PILING DATE: 2000-05
                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/207,727
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                                                                       Similarity
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                                                                                                                                                                                         PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICATION NUMBER: US/10/282,122A
AGGTACAGCCATGACTGCG 999
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Zamudio, Carlos
Malone, Cheryl
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Forsyth, R.
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                                                         Conservative
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RESULT 50

Application US/11097143

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PADDICANTON NO. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KITS
TITLE OF INVENTION: DETECTION EXPRESSION OF 10,000 OR MORE
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PRIOR FILING DATE: 2002-03-29
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PRIOR APPLICATION NUMBER: US 60/279,642
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 1040
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
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APPLICANT: Berg, Daniel J.
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLBIC ACID FOR TREATMENT OF NON-ALLERGIC TITLE OF INVENTION: INFLAMMATORY DISEASES
FILE REFERENCE: C1039.70060US01
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US-10-310-914A-779901
US-10-932-182A-66721
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US-11-021-492-370
US-09-925-065A-182610
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US-09-925-065A-354759
US-09-925-065A-354760
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US-11-124-368A-14151
US-11-124-367A-27765
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US-11-121-849-376206
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                                   Pred. No. 0.4
2; Mismatches
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                                                     DB 12; Length 20;
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                                     Indels
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Sequence 40214, A
Sequence 1665, Ap
Sequence 13774, A
Sequence 17155, A
Sequence 39967, A
Sequence 39967, A
Sequence 370, App
Sequence 182610,
Sequence 259573,
Sequence 259573,
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Sequence 380286,
Sequence 524783,
Sequence 321669,
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66721,
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                                     Gaps
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             RESULT 4
US-09-925-065A-73830
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RESULT 2 US-11-136-527-481

Sequence 73830, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single

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GENERAL INFORMATION:

APPLICANT: Wang, David G.

FITLE OF INVENTION: Identification and Mapping of Single

FITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome

FILE REPERENCE: 108827.135

FILE REPERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/247

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 5308
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-481
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US-09-925-065A-693333/c
                                                                                                                                                                         ; LENGTH: 605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-693333
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Publication No. US20050287570A1
GENERAL INFORMATION:
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                                                                                    Query Match
Best Local S
Matches 17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 693333
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APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OP INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
PRIOR PILING DATE: 2005-05-26
PRIOR FILING DATE: 2005-05-26
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                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-05-09
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||:||||||||||:|||
2734 GGTACAGCCAGGACTACG 2751
398 AGGCACAGCCAGGACTAAGA 379
                                                                                         17;
                                          1 AGGUACAGCCAGGACUACGA 20
                                                                                                            Similarity
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Pred. No. 10;
2; Mismatches
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Pred. No. 35;
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US-11-136-527-603; Sequence 603, App. Publication No.
                                                      RESULT 6
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Best Local
                                                                                                                                                                                  Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: _____Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/252,147 FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/261,766 FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/289,846
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 Application US/11136527 o. US20050287570A1
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Pred. No. 5
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Pred. No. 3
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SEQ ID NO 603
LENGTH: 1734
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                                                                                                                                                                            GENERAL INFORMATION:
                               CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                       TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum FILE.REFERENCE: 108827.135
                                                                                                                                                           APPLICANT: Wang,
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             G DATE: 2000-10-24
CATION NUMBER: US 60/252,147
                                                                                                                                                             David G.
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; ORGANISM: Rattus norvegicus US-11-136-527-603
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Best Local Similarity
Matches 14; Conser
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/330,773
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APPLICANT: Marc Malandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 031896-041000 CURRENT APPLICATION NUMBER: USCURRENT FILING DATE: 2005-05
                                                                                                                                                                                                                                                                                                                                                                                                               IIILE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
                                                                                                                                                                          LOCATION: (1)...(90616)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(90616
                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                              Local Similarity
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                                  3 GUACAGCCAGGACUAC 18
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GTACAGCCAGGACTAC 39985
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                                                                             Conservative
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                                                                                              Score 16; I
Pred. No. 1.
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Pred. No.
                                                                           Mismatches
                                                                                                                  DB 7;
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APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-36
PRIOR FILING DATE: 2001-01-36
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
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US-09-925-065A-132060
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US-09-925-065A-290636/c
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Best Local S
Matches 15
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                                                                                                                                                                 Sequence 290636, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
PILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILLING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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78.9%;
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78.9%;
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Pred. No. 1.2e
2; Mismatches
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Pred. No. 1.1e+02;
2; Mismatches 2
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1.2e+02;
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US-10-932-182A-77115

GENERAL INFORMATION:

APPLICANT: NAKAO,

NAKAO, YOSHIHIRO NAKAMURA, NORIHISA KODAMA, YUKIKO FUJIMURA, TOMOKO

APPLICANT:

APPLICANT:

Sequence 77115, Application US/10932182A Publication No. US20060046253A1

RESULT 12

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                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-925-065A-813093
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR TILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
PRIOR FILLING DATE: 2001-05-09
PRIOR FILLING DATE: 2001-05-09
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SEQ ID NO 290636
LENGTH: 533
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 813093
LENGTH: 572
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Best Local
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                                                                                                                         Query Match
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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ORGANISM: Homo sapiens
                                                                                                                                                                                                           TYPE: DNA
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Local Similarity 78.9%;
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  122 GGCACAGCCAGGACTAAGA 140
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                         2 GGUACAGCCAGGACUACGA 20
                                                                                                   h 79.0%;
Similarity 84.2%;
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                                                                                                       Score 15.8;
Pred. No. 1
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                                                                                      Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                  -10-330-773-713
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SEQ ID NO 77115
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                                                     3EQ ID NO 713
                                                                                                     FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS FILE REFERENCE: 030685-043
                                                                                                                                                         APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 197023
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CURRENT FILING DATE: 2004-09-02
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                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Saccharomyces pastorianus
ORGANISM: Mus musculus
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                      TYPE: DNA
                                   ENGTH: 43256
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                                                                      FastSEQ for Windows Version 4.0
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ASHIKARI, TOSHIHIKO
                                                                                                                                                                                                                                              Application US/10330773
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78.9%;
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Pred. No. 1
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Matches
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RESULT 16
US-09-925-065A-90145
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US-09-925-065A-173502
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hblication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20
                                                                                                             PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/250,092
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nes 16; Conserv
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Local Similarity 82.4%;
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                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/289,846
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                                                                 CATION NUMBER: US 60/289,846
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for Windows Version 4.0
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                                           2001-05-09
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84.2%;
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Pred. No. 1.
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Pred. No. 26
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-90145
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US-09-925-065A-90146
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                                                                                                                                                                                                                                                                                                                 Sequence 135672, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                          PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR ELING PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                               APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08
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                                     APPLICATION NUMBER: US 60/261,766
                                                         FILING DATE: 2000-11-30
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494 GGTACAGCCAGGACTCC 510
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14; Conservative 2; Mismatche
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                     2001-01-16
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82.4%;
US 60/289,846
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Pred. No. 1.
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Sequence 5, Application US/11121438

Publication No. US20060014173A1

PRICANT: Huang, Shi

PITTLE OF INVENTION: PR/SET- Domain Containing Nucleon of Invention: Polypeptides, Antibodies and PILE REFERENCE: P-LJ 5301

CURRENT APPLICATION NUMBER: US/11/121,438

CURRENT FILING DATE: 2005-05-03
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US-09-925-065A-768047
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US-11-121-438-5
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PRIOR FILLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
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Best Local Similarity 82.4
14; Conservative
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 135672
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
PILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
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                                       PRIOR APPLICATION NUMBER: US/10/200,012
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 09/910,478
PRIOR FILING DATE: 2001-07-18
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                        NUMBER OF SEQ ID NOS:
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Local Similarity 82.4%;
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FastSEQ for
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  Windows Version 4.0
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82.4%;
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Pred. No. 1.9e+02;
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Pred. No. 1.9e+02;
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and Methods of Use
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Best Local Similarity
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LENGTH: 2944
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                              CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                             APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIll00-1
                                                                                                                                                                           APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/437,482
               PRIOR APPLICATION NUMBER: US 60/437,482
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LOCATION: (250)...(1761)
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                                                                                                                                                                                                                              ence 56251, Application US/10750623 ication No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LICANT: FANTIN, Dennis
LE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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                                                                                                           ROSENFELD, David
HOLM, Tom
BATES, Stephen
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HOLM, Tom
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                                                                                                                                                             KERR, Richard
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DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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2002-12-31
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82.4%;
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88.2%;
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Pred. No. 2
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Pred. No. 2
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; ORGANISM: Homo sapiens
US-11-121-086-47
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US-11-121-086-47/c
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TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-591902
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Publication No. US20050266459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.
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ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Local Similarity 88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96035 TÁCAGCCAGGÁCTAGGA 96019
                                                                                                                                                        APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                   FILING DATE: 2000-11-30
                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/252,147 FILING DATE: 2000-11-20
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                                                                                               FastSEQ for Windows Version 4.0
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82.4%;
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Pred. No. 2.
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Pred. No. 3
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RESULT 25
US-09-925-065A-226237
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; ORGANISM: Homo sapiens
US-09-925-065A-226237
                                                                                                                                       FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma

FILE REFERENCE: 108827.135
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Best Local Similarity
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Best Local
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                        PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                       NUMBER OF SEQ ID NOS: 957086
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FastSEQ for Windows Version 4.0 20701
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Similarity 75.0%;
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75.0%;
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Pred. No. 2.4e+02;
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Pred. No. 2
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

FITLE OF INVENTION: Identification and Mapping of Single
FITLE OF INVENTION: Nuclectide Polymorphisms in the Human G
FILE REFERENCE: 108827, 135

CURRENT PILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925.065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
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US-09-925-065A-502873/c
Sequence 502873, Application US/09925065A
; Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-925-065A-191670
; Sequence 191670, Application US/09925065A
; Publication No. US20040181048A1
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SOFTWARE: PastSEQ for Windows
SEQ ID NO 502873
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PRIOR APPLICATION N
PRIOR FILING DATE:
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Local Similarity 80.0%;
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2001-05-09
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80.0%;
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Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.2; DB 6; Length 582;
Pred. No. 2.5e+02;
1; Mismatches 3; Indels
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; ORGANISM: Homo sapiens
US-09-925-065A-191670
                                                                                                                                                                                                                                                                                              US-10-467-657-2197
                                                                                                                                                                                                                                                                                                                       RESULT 30
                                                                                                                                                                                                                                    Sequence 2197, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Homo sapiens
-09-925-065A-544123
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                                                        CURRENT APPLICATION NUMBER: US/10/467,657
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                    PRIOR FILING DATE:
                                   PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
ITTLE OF INVENTION: Identification and Mapping of Single
ITTLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                  PPLICANT: CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence 544123, Application US/09925065A
blication No. US20040181048A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE:
                                                                                                                OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/252,147
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                                                                                                                                                                                                                                                                                                                                                                              AGGTGCAGCCAGGGCTAAGA 476
                                                                                                                                     PIZZA Mariagrazia
MASIGNANI Vega
MONACI Blisabetta
                                                                                                                                                                                                 FONTANA Maria Rita
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ID NOS: 9218
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75.0%;
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Pred. No. 2.
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Pred. No. 2
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US-09-925-065A-15531
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                                                                                                                                                                                                                                                                                                                                                                              SENERAL INFORMATION
                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                     CURRENT FILING DATE:
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                 UPPLICANT: Wang, David G.
ITTLE OF INVENTION: Identification and Mapping of Single
ITTLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                              equence 15531, Application US/09925065A
                                                                                                              APPLICATION NUMBER: US 60/261,766
                                                                                             [LING DATE: 2001-01-16
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FastSEQ for Windows Version 4.0

CATION NUMBER: US 60/289,846

2001-08-08

2001-05-09

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US-10-467-657-2199
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US-10-467-657-2199/c
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                                                                                                                                                                                                         SOFTWARE: Seq
SEQ ID NO 2199
                                                                                  Best Local Similarity
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2199, Application US/10467657 Publication No. US20050260581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FONTANA Maria Rita
                                                                                                                                                    TYPE: DNA ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                   TILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PIZZA Mariagrazia
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CHIRON SPA
                                                                                                                                                                                                                                                                                                                 TURRENT APPLICATION NUMBER: US/10/467,657
                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: MASIGNANI Vega
PPLICANT: MONACI Blisabetta
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                                                                                                                                                                                          ENGTH: 828
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793 AGGTACTGCCATGAATACGA 774
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                                AGGUACAGCCAGGACUACGA 20
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                                                                     Conservative
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                                                                                                                                                                                                                             version 1.04
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75.0%;
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75.0%;
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                                                                                    Score 15.2;
Pred. No. 2
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Pred. No. 2.
                                                                     Mismatches
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; NAME/KEY: misc feature
; LOCATION: (1)... (2049)
; OTHER INFORMATION: n = A,T,C
US-09-925-065A-15531
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; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-4937
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                                                                             ; LENGTH: 3090
TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-4937
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  Query Match
Best Local S
Matches 16
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Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4937, Application US/10932182A
Publication No. US20060046253A1
GENERAL INFORMATION:
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Publication No. US20060046253A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
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SEQ ID NO 4937
LENGTH: 3090
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APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAMA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SCOTMENDED: DECEMBER OF SEQ ID NOS: 197023
                                                                                                                                                        SEQ ID NO 4937
                                                                                                                                                                                             APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHKO
TITLE OP INVENTION: METHODS FOR ANALYZING GENES
FILE REFERENCE: 030685-043
FULCATION NUMBER: US/10/932,182A
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILLING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAO,
APPLICANT: NAKAMI
APPLICANT: KODAMI
                                                                                                                                                                            SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
/ Match 76.0%; Score 15.2; DB 7; Length 3090;
Local Similarity 80.0%; Pred. No. 3e+02;
nes 16; Conservative 1; Mismatches 3; Indels 0
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KODAMA, YUKIKO
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75.0%;
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Pred. No. 2.9e+02;
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                                                                                                                                                                                                                                                                              OF INDUSTRIAL YEASTS
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FILE REFERENCE: 529452001300

CURRENT APPLICATION NUMBER: US/10/330,773

CURRENT FILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 981

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 511

LENGTH: 58687

TYPE: DNA

ORGANISM: Mus musculus
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US-10-330-773-620/c
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US-10-330-773-511/c
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Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 620, Application US/10330773 Publication No. US20060040262A1
                                                                                                                                                                                                                                                                                        SEQ ID NO 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                   Matches
                                                                                                     Query Match
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LOCATION: (1)...(58687)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(100137)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                   ENGTH: 100137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 76.0%;
Local Similarity 80.0%;
                                                                                      Match 76.0%;
Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17509 AGGAAAAGCCAGGACTACAA 17490
5669 AGATACAGCCAGTACTACCA 5650
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                                 1 AGGUACAGCCAGGACUACGA 20
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                                                                     Conservative
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Pred. No. 4.4e+02;
                                                                                      Score 15.2; DB 7; Pred. No. 4.7e+02;
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                                                                       Mismatches
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                                                                                                       Length 100137;
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                                                                         Gaps
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RESULT 37 US-10-995-561-13330/c

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Sequence 13330, Application US/10995561 Publication No. US20050272054A1

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; NAME/KRY: misc_feature ; LOCATION: (1)...(101046) ; LOCATION: (1)...(101046) ; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1.US-10-995-561-13330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-330-773-76/c
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Best Local Similarity 75.0
15; Conservative
                                                                                                                                                                                                                             Sequence 1, Application US/11091018 Publication No. US20050287551A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENERAL INFORMATION:
                              FILE REFERENCE: 2345.2010-016
CURRENT APPLICATION NUMBER: US/11/091,018
CURRENT FILING DATE: 2005-03-25
                                                                                            APPLICANT: Gretarsdottir, Solveig
APPLICANT: Thorleisson, Gudmar
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
                                                                                                                                                                                                            ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQ ID NO 76
LENGTH: 118544
TYPE: DNA
               PRIOR APPLICATION NUMBER: PCT/US03/29906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 85702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/995,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                      16256 AGGCACAGCCAGGACTGTGA 16237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53538 AGGTACACACAGGACTAAGA 53519
                                                                                                                                                                                                                                                                                                                                                                                                                                     76.0%;
l Similarity 80.0%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10330773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RE
2003-09-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morris
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75.0%;
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Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.2;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 118544;
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; TYPE: DNA
; ORGANISM: homo sapien
US-11-175-859-84034
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                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 11625;
SOFTWARE: PatentIn version :
SEQ ID NO 84034
                                                                         Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 84034, Application US/11175859 Publication No. US20060024715A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et
                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 3690.
                                                                                                                                                                                                                                                                                                                                                                     RPPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/811,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)...(1691140)
OTHER INFORMATION: n=A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734050 AGGTACAGCCAAGACTGGGA 734069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2002-09-25
APPLICATION NUMBER: 10/419,723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2002-02-04
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19
                                                                       13;
                                1 AGGUAÇAGÇÇAGGAÇUA 17
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ATGTACARCCAGGACTA 35
                                                                       Conservative
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                                                                                      75.0%;
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75.0%;
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Pred. No. 5.3e
2; Mismatches
                                                                                      Score 15;
Pred. No. 2
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                                                                                                     Length 50;
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Sequence 16998, Application US/11124368A Publication No. US20050287559A1

11-124-368A-16998

GENERAL INFORMATION:

APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detect

Detection and Uses Thereof

ILE REFERENCE: CL001524

ICATION NUMBER: US/11/124,368A

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; ORGANISM: Homo sapiens
US-11-124-368A-16998
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-66
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-05-09
PRIOR PILING DATE: 2001-01-05-09
PRIOR PILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                     RESULT 43
US-09-925-065A-793457
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; ORGANISM: Homo sapiens
US-09-925-065A-439000
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PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 439000, Application US/09925065A Publication No. US20040181048A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 439000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                    Sequence 793457, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
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414 GGTACAGCCAGGACT 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGUACAGCCAGGACU 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 75.0%; Score 15; DB 6; Length 475; Similarity 86.7%; Pred. No. 3.1e+02;
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76.5%;
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Pred. No. 2.8e+02;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 201;
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                                                                                                                                                        Human Genome
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,766
PRIOR APPLICATION NUMBER: US 60/261,766
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; ORGANISM: Homo sapiens
US-09-925-065A-793457
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US-09-925-065A-361014/c
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 793457
LENGTH: 506
                                                                                                                                                                                                                                                            RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: FASTSI
SEQ ID NO 361014
LENGTH: 532
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                          GENERAL INFORMATION:
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Best Local &
                                                                                                                                                                             Sequence 361016, Application US/09925065A Publication No. US20040181048A1
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 75.0%; Score 15; DB 6; Cocal Similarity 93.3%; Pred. No. 3.1e+02;
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86.7%;
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Pred. No. 3.1e+02;
2; Mismatches 0
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                                                                                          Human Genome
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APPLICATION NUMBER: US 60/243,096

FILING DATE:

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US-09-925-065A-178453
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US-09-925-065A-361019/c
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                                                                                                                     RESULT 47
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US-09-925-065A-361019
                                                      GENERAL
                                                                 Sequence 178453, Application US/09925065A Publication No. US20040181048A1
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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                 ITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                        ENGTH:
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ORGANISM: Homo sapiens
     TLE OF INVENTION:
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FILING DATE: 2000-11-30
APPLICATION NUMBER: US 60/261,766
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FILING DATE: 2000-11-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/289,846
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FILING DATE: 2000-11-30
APPLICATION NUMBER: US 60/261,766
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                                                    INFORMATION
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Similarity 93.3%;
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                                    David G.
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Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
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93.3%;
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Pred. No.
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US-09-925-065A-361018/c

Sequence 361018, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:

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SEQ ID NO 361017
                                                                        Matches
                                                                                             Query Match
Best Local Similarity
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SEQ ID NO 178453
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PRIOR FILING DATE: 2000-11-20
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PRIOR APPLICATION NUMBER: US 60/243,096
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.135
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PRIOR APPLICATION NUMBER: US 60/252,147
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les 13; Conserv
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                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/261,766 FILING DATE: 2001-01-16
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APPLICATION NUMBER: US 60/250,092
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252 AGGTÁCAGCCAGGAC 238
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                                                                          14;
                                    1 AGGUACAGCCAGGAC 15
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                                                                          Conservative
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                                                                                             93.3%;
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                                                                                             Score 15; |
Pred. No. 3
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Pred. No.
                                                                          Mismatches
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                                                                                               .1e+02
                                                                                                           Length 577
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TILE OF INVENTION INVEST: 2001-08-08
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/251,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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SEQ ID NO 361018
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-361018
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 636833
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                                                                                                                                                                                                                              ; LENCTH: 638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-636833
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                                                                                                    Query Match 75.0%; Score 15; DB 6; Length 638; Best Local Similarity 93.3%; Pred. No. 3.2e+02; Matches 14; Conservative 1; Mismatches 0; Indels
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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